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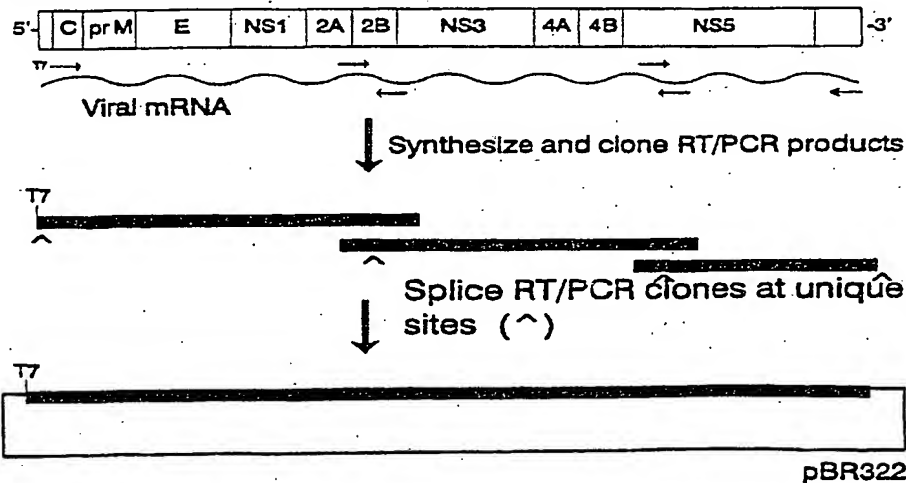
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Chimeric
DENV-2 viruses!

(54) Title: INFECTIOUS DENGUE 2 VIRUS PDK-53 AS QUADRAVALENT VACCINE

Construction of DEN-2 Infectious cDNA Clone



(57) Abstract

The invention relates to infectious cDNA clones for Dengue 2 virus, strain 16681, and its live, attenuated vaccine derivative, PDK-53 (DEN-2 PDK-53). The invention also relates to infectious cDNA clones for chimeric viruses characterized as expressing structural genes of a Dengue 1, Dengue 3, or Dengue 4 attenuated virus in the context of the nonstructural genes of the Dengue 2 PDK-53 virus (DEN-2/1, DEN-2/3, DEN-2/4). The invention further relates to genetic constructs encoding these cDNAs, and host cells containing these constructs. The invention moreover relates to quadravalent vaccines providing immunity against all four serotypes of dengue virus comprising DEN-2 PDK-53 infectious clone derivative, DEN-2/1, DEN-2/3, or DEN-2/4 viruses, and related methods of immunization.

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INFECTIOUS DENGUE 2 VIRUS PDK-53 AS QUADRAVALENT VACCINE

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Field of the Invention

The invention relates to infectious cDNA clones for Dengue 2 virus, strain 16681, and its live, attenuated vaccine derivative, PDK-53 (DEN-2 PDK-53). The invention
10 also relates to infectious cDNA clones for chimeric viruses characterized as expressing structural genes of a Dengue 1, Dengue 3, or Dengue 4 attenuated virus in the context of the nonstructural genes of the Dengue 2 PDK-53 virus (DEN-2/1, DEN-2/3, DEN-2/4). The invention further
15 relates to genetic constructs encoding these cDNAs, and host cells containing these constructs. The invention moreover relates to quadravalent vaccines providing immunity against all four serotypes of dengue virus comprising DEN-2 PDK-53 infectious clone derivative, DEN-
20 2/1, DEN-2/3, or DEN-2/4 viruses, and related methods of immunization.

Background of the Invention

Arthropod-borne viruses (arboviruses) are a diverse
25 group of viruses that have been lumped together on the basis of their ecological niche, which involves cycles of transmission between vertebrate hosts and arthropod vectors such as mosquitos and ticks. The prototype arbovirus is yellow fever virus, a flavivirus, which was
30 isolated in 1927. In the 1950s, the Rockefeller Foundation established a number of field stations in

various tropical countries for the purpose of isolating new viruses. The 1985 International Catalogue of Arboviruses Including Certain Other Viruses of Vertebrates contains registrations for 504 discrete arboviruses, 124 of which have caused disease in humans. Thirty-four viruses of the Flavivirus genus (family Flaviviridae) of arboviruses are human pathogens (Karabatsos, 1985). (All publications cited hereunder are incorporated herein by reference.)

According to a 1992 World Health Organization (WHO) press release (Press Release WHO/74, November 24, 1992), dengue hemorrhagic fever is one of the most important and increasing mosquito-transmitted infections in the world, with more than 85 countries in Asia, the Pacific Islands, Africa, Central America, and South America being threatened with dengue outbreaks. Dengue fever was known in the past as "breakbone fever" due to the severe muscular and joint pain that accompanied the high fever during this infection. Dengue is an under-reported disease: it is thought that millions of cases occur each year.

Dengue (DEN) viruses, which are flaviviruses, are classified antigenically into 4 serotypes (DEN-1, DEN-2, DEN-3, and DEN-4). Multiple serotypes are now endemic in most countries in the tropics. DEN viruses are transmitted to humans principally by *Aedes aegypti* mosquitos throughout much of the tropical and subtropical region of the world. Viruses of all four serotypes infect humans and cause clinically inapparent infection or illness ranging from dengue fever to severe and often

fatal dengue hemorrhagic fever/dengue shock syndrome (DHF/DSS). DHF/DSS has been associated epidemiologically and experimentally with immune enhancement of virus replication by preexisting, subneutralizing levels of heterotypic antibody. About 90% or more of patients with DHF/DSS are children who are 14 years old or younger (Halstead, 1970; Halstead, 1988). Case fatality rates in untreated individuals can be as high as 15-20%. Between 1956 and 1978, hospitalization of more than 350,000 dengue patients and about 12,000 deaths in Southeast Asia were reported to the WHO (Halstead, 1980). More recent dengue epidemics in Asia, the Pacific islands, the Americas, and Africa indicate that the incidence, with up to 40 million cases annually, and geographic distribution of the disease is increasing in *Aedes aegypti*-infested areas of the world (Halstead, 1984; Gubler, 1988; Brandt, 1990).

Since eradication of *Aedes aegypti* mosquitos appears to be practically infeasible, development of safe, effective vaccines against all four serotypes of DEN virus is a WHO priority (Gubler, 1988; Brandt, 1988; Brandt, 1990). Since the level of DEN virus replication in certified cell cultures yields insufficient antigenic mass to produce effective inactivated vaccines, priorities are given to developing effective live, attenuated vaccine viruses and using a variety of expression systems such as recombinant vaccinia or avipox virus (live vaccine), recombinant baculovirus (subunit vaccine), and recombinant *E. coli* (subunit vaccine) to express certain genes of the DEN viral genome (Brandt, 1988; Brandt, 1990).

Flaviviruses are enveloped RNA viruses 45 to 50 nm in diameter that contain a single-stranded, positive-sense capped RNA genome of approximately 11 kb. The RNA genome does not have a 3'-terminal poly(A) tail. Because the genetic molecule of flaviviruses is positive or messenger RNA (mRNA)-sense, naked genomic RNA injected, transfected, or electroporated into mammalian or invertebrate cells is capable of associating directly with the ribosomal protein synthetic machinery of the cell. All of the viral proteins are translated from the inserted viral genomic mRNA. These virus-specified proteins then replicate the viral genome, resulting in intracellular virus maturation and release of infectious virus from the transfected cell.

The gene organization of the flavivirus mRNA genome, illustrated below, is 5'-noncoding region (5'-NC)-capsid-premembrane/membrane (prM/M)-envelope (E)-nonstructural protein 1 (NS1)-NS2A-NS2B-NS3-NS4A-NS4B-NS5-3'-noncoding region (3'-NC). The structural proteins capsid, prM/M, and E and nonstructural proteins are translated as a large precursor polyprotein molecule from a single long open reading frame in the mRNA genome. The individual mature viral proteins are processed from the polyprotein by both cell and virus specified proteases (Westaway et al., 1985; Coia et al., 1988; Speight and Westaway, 1989; Rice et al., 1985).

Genome Organization of Dengue Virus and Other Flaviviruses

	C	M	E	NS1	2A	2B	NS3	4A	4B	NS5	3'-NC
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The structural proteins are those viral proteins that are incorporated into the mature virion. The virion consists of an icosahedral capsid (C) that packages the viral genomic mRNA (nucleocapsid). The nucleocapsid is surrounded by a cell-derived lipid membrane into which the envelope (E) and mature membrane (M) proteins are imbedded. The virus-specific nonstructural genes, NS1-NS5, are expressed in the cytoplasm of the infected cell and are involved in the replication and maturation of the viral RNA genome and viral proteins.

The E glycoprotein of the virus is exposed to the environment and is involved in attachment and entry of the virus into the cell. The E protein is the primary viral immunogen against which the infected vertebrate host develops virus-specific neutralizing antibody. The E gene is the most common target for development of molecular systems to express the encoded E glycoprotein. However, immunization with various purified nonstructural genes of the virus have been shown to elicit protective immunity against challenge with wild-type virus, probably via cytotoxic T-cell mediated lysis of infected cells which express viral nonstructural proteins on the cell surface.

Vaccination can be one of the most cost effective ways to prevent dengue fever and DHF/DSS. Since 1979 the WHO has supported research on dengue vaccine development at the Mahidol University in Bangkok, Thailand (Press Release WHO/74, November 24, 1992). Investigators at Mahidol University have developed four live, attenuated candidate vaccine viruses, one for each of the four serotypes, by serial passage of the virulent parent

viruses in primary dog kidney (PDK) or fetal rhesus lung (FRhL) cell culture (Yoksan et al., 1986; Bhamarapavati et al., 1987). Phase 1 and Phase 2 clinical trials in Thailand have demonstrated that the vaccine is both safe and immunogenic in humans. The vaccines now need to be tested for efficacy in large numbers of children (Press Release WHO/74, November 24, 1992). To preclude the possible severe DHF/DSS immune enhancement phenomenon in vaccinees who might be infected naturally with a heterologous serotype of wild-type DEN virus following immunization with a single serotype of vaccine virus, it is essential that humans be vaccinated with a quadravalent vaccine to provide immunity against all four serotypes of the virus.

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Summary of the Invention

The invention provides a quadravalent vaccine providing immunity against all four serotypes of dengue virus comprising a DEN-2 PDK-53 infectious clone-derived virus.

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The invention also provides a quadravalent vaccine providing immunity against all four serotypes of dengue virus comprising a chimeric DEN-2/1 virus.

The invention further provides a quadravalent vaccine providing immunity against all four serotypes of dengue virus comprising a chimeric DEN-2/3 virus.

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The invention moreover provides a quadravalent vaccine providing immunity against all four serotypes of dengue virus comprising a chimeric DEN-2/4 virus.

The invention additionally provides a quadravalent vaccine providing immunity against all four serotypes of dengue virus comprising DEN-2 PDK-53 infectious clone-derived and chimeric DEN-2/1, DEN-2/3, and DEN-2/4 viruses.

In another aspect, the invention provides a method of immunization in which a desired immune response is produced against all four serotypes of dengue virus comprising the step of administering to a subject a quadravalent vaccine comprising DEN-2 PDK-53 infectious clone-derived and chimeric DEN-2/1, DEN-2/3, and DEN-2/4 viruses.

In yet another aspect, the invention provides a composition of matter comprising a full genome-length infectious cDNA clone for a DEN-2 virus, strain 16681.

The invention also provides a composition of matter comprising a full genome-length infectious cDNA clone for a DEN-2 virus of a strain characterized as replicating to high titer in cell culture.

The invention further provides a composition of matter comprising a full genome-length infectious cDNA clone for a DEN-2 virus, strain 16681, having the identifying characteristics of ATCC 69826.

In still another aspect, the invention provides a composition of matter comprising a full genome-length infectious cDNA clone for a DEN-2 virus, strain 16681, attenuated derivative, PDK-53.

The invention also provides a composition of matter comprising a full genome-length infectious cDNA clone for a DEN-2 virus attenuated derivative,

characterized as replicating to high titer in cell culture.

The invention further provides a composition of matter comprising a full genome-length infectious cDNA
5 clone for a DEN-2 virus, strain 16681, attenuated derivative, PDK-53, having the identifying characteristics of ATCC 69825.

In another aspect, the invention provides a composition of matter comprising a full genome-length
10 infectious cDNA clone of a chimeric DEN-2/1 virus, wherein the virus is characterized as expressing the prM and E genes of a DEN-1 attenuated virus in the context of the nonstructural genes of the DEN-2 PDK-53 virus. The DEN-1 attenuated virus may be DEN-1 PDK-13.

15 The invention also provides a composition of matter comprising a full genome-length infectious cDNA clone of a chimeric DEN-2 virus, wherein the virus is characterized as expressing the antigenicity of a DEN-1 attenuated virus.

20 In yet another aspect, the invention provides a composition of matter comprising a full genome-length infectious cDNA clone of a chimeric DEN-2/3 virus, wherein the virus is characterized as expressing the prM and E genes of a DEN-3 attenuated virus in the context of the
25 nonstructural genes of the DEN-2 PDK-53 virus. The DEN-3 attenuated virus may be DEN-3 PGMK30/FRhL-3.

The invention also provides a composition of matter comprising a full genome-length infectious cDNA clone of a chimeric DEN-2 virus, wherein the virus is

characterized as expressing the antigenicity of a DEN-3 attenuated virus.

In still another aspect, the invention provides a composition of matter comprising a full genome-length infectious cDNA clone of a chimeric DEN-2/4 virus, wherein
5 the virus is characterized as expressing the prM and E genes of a DEN-4 attenuated virus in the context of the nonstructural genes of the DEN-2 PDK-53 virus. The DEN-4 attenuated virus may be DEN-4 PDK-48.

10 The invention also provides a composition of matter comprising a full genome-length infectious cDNA clone of a chimeric DEN-2 virus, wherein the virus is characterized as expressing the antigenicity of a DEN-4 attenuated virus.

15 Additionally, the invention provides a genetic construct comprising a DNA sequence operably encoding the polyprotein of DEN-2 virus, strain 16681. The polyprotein may be the polyprotein encoded by the nucleotide sequence of SEQ ID NO:1.

20 The invention also provides a genetic construct comprising a DNA sequence operably encoding at least one protein of DEN-2 virus, strain 16681. The protein may be a protein encoded by the nucleotide sequence of SEQ ID NO: 1.

25 Further, the invention provides a genetic construct comprising a DNA sequence operably encoding the polyprotein of DEN-2 virus, strain 16681, attenuated derivative, PDK-53. The polyprotein may be the polyprotein encoded by the nucleotide sequence of SEQ ID
30 NO:2.

The invention also provides a genetic construct comprising a DNA sequence operably encoding at least one protein of DEN-2 virus, strain 16681, attenuated derivative, PDK-53. The protein may be a protein encoded by the nucleotide sequence of SEQ ID NO: 2.

Moreover, the invention provides a genetic construct comprising a DNA sequence operably encoding at least one structural protein of DEN-1 PDK-13. The structural protein may be a structural protein encoded by the nucleotide sequence of SEQ ID NO: 124.

In another aspect, the invention provides a genetic construct comprising a DNA sequence operably encoding at least one structural protein of DEN-3 PGMK30/FRhL-3. The structural protein may be a structural protein encoded by the nucleotide sequence of SEQ ID NO: 125.

In still another aspect, the invention provides a genetic construct comprising a DNA sequence operably encoding at least one structural protein of DEN-4 PDK-48. The structural protein may be a structural protein encoded by the nucleotide sequence of SEQ ID NO: 126.

In yet another aspect, the invention includes a host cell comprising any of the above genetic constructs.

Brief Description of the Drawings

Figure 1: Strategy for construction of the full genome-length cDNA clone of DEN-2 virus. Using PCR technology, cDNA is amplified from the genomic RNA of the virus and cloned. Subclones are spliced together at unique, overlapping restriction enzyme sites to construct

the full genome-length clone. Numbered arrows upstream (right arrows) and downstream (left primers used to amplify the cDNA in PCR reactions.

Figure 2: Transcription of genomic mRNA from the full-length infectious cDNA clone of DEN-2 virus. The recombinant plasmid is linearized at the unique XbaI site at the 3'-end of the genomic cDNA. Bacteriophage T7 RNA polymerase recognizes the T7 promoter engineered at the 5'-end of the cDNA and transcribes full-length viral mRNA from the cDNA template.

Figure 3: Restriction enzyme sites identified in the nucleotide sequence of the RNA genome of DEN-2 16681 virus. Locations for the sites are indicated by the genome nucleotide numbers. Restriction enzymes that cleave the DEN-2 genomic cDNA at only a single location are listed vertically at the top of the figure. The resolution of the RENZ graph is 97.5 nucleotides per dot.

Figure 4: Growth curve of DEN-2 16681 virus in C6/36 mosquito cells.

Figure 5: (A) Polaroid prints showing RT/PCR amplification of the entire mRNA genome of DEN-2 virus, strain 16681, in the form of 5 cDNA amplicons. The molecular weight marker (MW) consists of linear, double-stranded DNA markers of various base pair (bp) lengths. The top 2 gels show 5- μ l aliquots of the original RT/PCR reactions. The bottom two gels show 10% of the yield following HMC agarose gel purification of the remaining 95- μ l reaction aliquots. (B) Primers (amplimers) used in the RT/PCR reactions and the expected sizes of the resulting cDNA amplicons.

Figure 6: EcoRI restriction enzyme digests of F2, F2-Sal, Sal-F2, and F3 miniprep recombinant plasmid DNA. Plasmids from individual colonies resulting from transformation with independent ligated, recombinant plasmid molecules are numbered. The insert in the single F2-8 plasmid was too small and was discarded. The remaining recombinant plasmids contained cDNA inserts of expected size. As expected, F2-Sal cDNA contained two internal EcoRI sites; the Sal-F2 and F3 plasmids contained a single internal EcoRI site. EcoRI digestion of the recombinant plasmids regenerated linearized, wild-type 3.9-kb pCRII vector. For an undetermined reason, one of the EcoRI sites in plasmid F3-1 did not cut.

Figure 7: Schematic diagram showing the genomic locations of DEN-2 16681 virus-specific cDNA clones. Clones indicated with asterisks were spliced together at the indicated restriction enzyme sites to construct the full genome-length cDNA clone. Black horizontal bars indicate clone regions that were sequenced. Light gray regions of horizontal bars indicate clone regions that were not sequenced.

Figure 8: (A) Effect of adding Taq extender reagent to PCR reactions. The 5.2-kbp amplicon of St. Louis encephalitis virus was readily obtained by extended PCR (+) but not by standard PCR (-). (B) Agarose gel electropherogram showing DEN-2 PDK-53 F1, F2, and F3 amplicons derived by extended PCR.

Figure 9: Schematic diagram showing the genome locations of errors identified in the cDNA clones of DEN-2 16681. Errors are indicated by short vertical tick marks.

Figure 10: Schematic diagram illustrating the approximate genome locations of the nucleotide discrepancies between the data of Applicants and those of Blok et al. (1992) for the sequence of the genome of DEN-2 virus, strain 16681.

Figure 11: Nucleotide sequence of the genome of DEN-2 strain 16681 virus. Differences between the data determined by Blok et al. (1992) (DEN-2-16681.BLOK) and those obtained by Applicants (DEN-2-16681.RK). The genome nucleotide positions of the sequence differences are listed vertically. The solid squares indicate those nucleotide differences that also encode amino acid substitutions. The remaining nucleotide differences are either silent, encoding the same amino acid, or lie within the 5'-noncoding (5'-NC) or 3'-noncoding region (3'-NC).

Figure 12: Schematic diagram showing the DEN-2 PDK-53 virus-specific cDNA clones and the approximate locations of cDNA errors (vertical tick marks) identified by nucleotide sequence analyses. Clones marked with an asterisk were used in the construction of the DEN-2 PDK-53 virus-specific full-length cDNA clone. Clone #19 had a 203-bp deletion (horizontal line).

Figure 13: Schematic summary of the DEN-2 16681 vs. PDK-53 virus sequencing projects. Arrows indicate the nucleotide differences detected between the two genomes. Triangles indicate those nucleotide changes that resulted in amino acid substitutions.

Figure 14: Finalized nucleotide and amino acid sequence of the RNA genome of DEN-2 virus, strain 16681 (SEQ ID NO:1). The nucleotide and amino acid mutations

that were determined to have occurred in DEN-2 virus, strain PDK-53, are indicated at the appropriate positions (SEQ ID NO:2). The EcoRI, SstI, MuiI, and T7 promoter sites that were engineered immediately preceding the 5'-terminal nucleotide of the virus-specific genomic cDNA are shown. The start positions of the viral genes and noncoding regions (5'-NC and 3'-NC) are shown. Potential sites of Asn-linked glycosylation (Asn-X-Ser or Thr, where X = any amino acid) in prM, E, and NS1 are indicated by asterisks. The deduced amino acid sequence is indicated in standard single-letter abbreviation: A = Ala, C = Cys, D = Asp, E = Glu, F = Phe, G = Gly, H = His, I = Ile, K = Lys, L = Leu, M = Met, N = Asn, P = Pro, Q = Gln, R = Arg, S = Ser, T = Thr, V = Val, W = Trp, Y = Tyr.

Figure 15: Construction of intermediate clone F2 by ligating the F2-Sal SphI/HpaI fragment and Sal-F2 HpaI/KpnI fragment into pUC18. The resulting F2 clone contained a nonsilent cDNA error at genome nucleotide position 1730.

Figure 16: Correction of the intermediate F2 clone. A new PCR amplicon was cloned and sequenced. The SphI/HpaI fragment of this clone was spliced into F2 to construct F2-C having the correct nucleotide at genome position 1730.

Figure 17: Construction of the intermediate F1/3/4/5 cDNA clone for DEN-2 16681 virus. The thick solid black bars indicate DEN-2 virus-specific cDNA, illustrated with the RENZ sites of the MCS of the plasmid. The RENZ sites used in each step of the splicing strategy are indicated in underlined, bold characters. The top half of the

figure shows construction of F1/3/4/5-pUC18. The bottom portion of the figure illustrates the making of F1/3/4/5-pUC19. The final step in the construction of the full genome-length cDNA clone involved the ligation of the F2-C SphI/KpnI cDNA fragment into plasmid containing cDNA F1/3/4/5 and cut with RENZs SphI/KpnI. Although F2-C cDNA could not be cloned into F1/3/4/5-pUC18, it was readily cloned into F1/3/4/5-pUC19. The pUC18 plasmid containing a small insert of cDNA made for Venezuelan equine encephalitis (VEE) virus was used simply to move F1 and F4/5 into pUC18 in a 3-molecule ligation reaction. The VEE virus-specific cDNA was spliced out during this process. Arrowheads under cDNA bars indicate orientation of mRNA-sense cDNA strand.

Figure 18: Orientation specific cloning of full genome-length cDNA of DEN-2 16681 virus into the multiple cloning site of pUC19. Although the full-length cDNA was readily cloned in pUC19, multiple attempts to insert the cDNA into pUC18 failed. Presumably, interaction of the cDNA with pUC18-specific gene transcripts, translation of a toxic DEN-2 polypeptide, or translation of a toxic pUC18/DEN-2 fusion polypeptide produced deleterious effects in *E. coli*. Large arrows indicate orientation of mRNA-sense cDNA strands in the pUC plasmid backbone. Smaller arrows indicate orientations of the *lac Z* and ampicillin genes as well as the origin of replication. DEN-2 insert is indicated by a thick solid black line.

Figure 19: Insertion of the MCS of plasmid pUC19 into pBR322 in both orientations to construct pBRUC-138 and pBRUC-139. The pUC18 HindIII (blunt-ended = BL)/EcoRI

MCS fragment was ligated into pBR322 cut with *Ava*I (BL)/*Eco*RI to construct pBRUC-138. The pUC18 *Eco*RI (BL)/*Hind*III MCS fragment was ligated into pBR322 cut with *Ava*I (BL)/*Hind*III to make pBRUC-139. In both cases, the tetracycline gene of pBR322 was removed. pBRUC-138 = 2992-bp (61-bp MCS + 2931-bp pBR322 deletion vector). pBRUC-139 = 3022-bp (61-bp MCS + 2961-bp pBR322 deletion vector). Orientations of ORI, ROP, and the Amp gene are indicated.

10 **Figure 20:** Construction of pD2/IC-30P, the full genome-length cDNA clone of DEN-2 16681 virus, in plasmid pBR322 (pBRUC-139 (*Sph*I-) derivative). The F3/4/5 clone cDNA was ligated into pBRUC-139 first (Top of Figure), followed by F1-E and F2-C. Viable, infectious DEN-2 virus was successfully obtained from viral mRNA transcribed from this clone.

15 **Figure 21:** Construction of pD2/IC-130V, the full genome-length cDNA clone of DEN-2 PDK-53 virus. A nonsilent error in cDNA clone F3-3C was corrected by splicing in a correct *Bst*BI/*Nhe*I fragment from clone F3.5-6 (Top). The resulting corrected clone F3-3CC was spliced into the 16681 F345-F clone in pBRUC-139. cDNA fragments F1-79B, F2-16B, and the recombinant F3/4/5 vector DNA were spliced together in a single ligation reaction to produce pD2/IC-130V. The *Nhe*I site occurs at genome nucleotide position 6646. Therefore, the PDK-53 virus-specific full-length cDNA clone contains the parental 16681 virus-specific nucleotide at position 8571. This nucleotide difference is silent; it does not encode an amino acid change. Other than the 8571 position, DEN-2 16681 and

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PDK-53 viruses are identical in nucleotide sequence from nucleotide position 6646 to the 3' terminus of the genome.

Figure 22: Agarose gel electropherogram of viral genomic mRNA extracted from gradient-purified, wild-type DEN-2 16681 virus and Venezuelan equine encephalitis (VEE) virus. The quantity of RNA loaded onto the gel ranged from 22 ng to 383 ng. The stock RNA was quantitated spectrophotometrically at 260 nm. The genome-length RNA band is clearly visible between the 4153-bp and 6788-bp MW marker bands. Bands were visualized by incorporating 200 ng/ml of ethidium bromide stain in the gel and electrophoresis buffer.

Figure 23: Transcription of RNA from pVE/IC-92 (VEE virus clone) and pD2/IC-20 (DEN-2 16681 virus clone). Transcription reaction conditions (100 ng linearized DNA template, 12.5 mM DTT, 2.7 u/ μ l RNasin, 0.15 mM NTPs, 3.3 U/ μ l T7 RNA polymerase (Stratagene) in commercial buffer (Stratagene)) yielded high quantity and quality of infectious mRNA transcripts from the pVE/IC-92 clone and 3'-end truncation products of that clone. However, these reaction conditions failed to permit transcription of RNA from the pD2/IC-20 clone or two of its 3'-end transcription products (clone linearized at the NsiI or MroI site instead of at the 3'-terminal XbaI site). pVE/IC-92 plasmid linearized at the MluI (3'-terminal), SphI, Tth111I, HindIII, SalI, and StuI sites in the cDNA clone yielded RNA transcripts of 11447, 11377, 7541, 2407, 1620, and 674 base length, respectively (the more intense, prominent bands in these gel lanes).

Figure 24: Transcription of RNA from the DEN-2 16681 cDNA clone pD2/IC-20. (A) Transcription of RNA using different quantities of linearized plasmid template (a,b). The cap analog m7G(5')ppp(5')A was not included in the reaction. (B) Transcription of 5'-capped RNA with inclusion of cap analog in the reaction. Transcription was accomplished with the Ampliscribe transcription kit from Epicentre Technologies. T7 pol = bacteriophage T7 RNA polymerase.

Figure 25: Transcription of full genome-length, infectious viral mRNA from XbaI-linearized DEN-2 16681 plasmid pD2/IC-30P (A and D replicate clones resulting from independent bacterial colonies transformed with the recombinant pBRUC/DEN-2 plasmid) and PDK-53 plasmid pD2/IC-130V (F and J replicates). Genomic "viral RNA" extracted from gradient-purified wild-type DEN-2 16681 virus was electrophoresed in lanes 2 and 10. Aliquots of transcription reactions sampled before (T7 RNA polymerase "-") and after (T7 Pol "+") addition of T7 RNA polymerase are shown. Only the linearized plasmid DNA template is observed in the absence of the polymerase.

Figure 26: Transcription of RNA from pD2/IC-20, pD2/IC-30P, and pD2/IC-130V in the presence or absence of T7 RNA polymerase or cap analog in the transcription reaction. All lanes shown are on a single gel. Transcription was performed with the Ampliscribe transcription kit.

Figure 27: Derivation tree for the construction of the DEN-2 16681 and PDK-53 virus-specific full genome-length cDNA clones pD2/IC-30P and pD2/IC-130V,

respectively, and chimeric 16681/PDK-53 clones derived from the two prototype clones.

Figure 28: Genotype maps of DEN-2 16681 and PDK-53 virus-specific full genome-length cDNAs and their chimeric derivatives. The scale at the top indicates relative genome nucleotide position in thousands. The graph resolution is 119.1444 bp/dot. cDNA regions contributed by the parental DEN-2 16681 virus are indicated by solid black bars. Regions derived from the DEN-2 PDK-53 vaccine virus are indicated by stippled bars. The 8 mutations identified by sequence analyses of the genomes of the 16681 and PDK-53 viruses are indicated. The virus-specific 5-noncoding nucleotides are indicated in lower case characters. The amino acids encoded by the virus-specific nucleotide mutations in the protein coding region of the genome are indicated in upper case, single-letter amino acid abbreviation.

Figure 29: Results of spot-sequencing PCR amplicons amplified from seed stocks of viruses derived from full genome-length cDNA clones. Dots indicate nucleotide sequence identity to the DEN-2 16681 virus. The expected virus-specific nucleotides for the genotype of each virus are shown. Those nucleotide positions that have actually been confirmed by sequence analysis are indicated by underlined nucleotide base characters. The actual genome nucleotide positions are indicated at the bottom of the Figure.

Figure 30: Recombinant full-length pD2/IC-30P-A and pD2/IC-130V-F plasmids extracted from 1-ml aliquots of *E. coli* TB-1 cultures submitted to ATCC.

Figure 31: Partial nucleotide sequences of candidate vaccine viruses:

DEN-1 16007 PDK-13	(D1.VAC) (SEQ ID NO: 124)
DEN-2 16681 PDK-53	(D2.VAC) (<u>see</u> SEQ ID NO: 2)
5. DEN-3 16562 PGMK-30/FRhL-3	(D3.VAC) (SEQ ID NO: 125)
DEN-4 1036 PDK-48	(D4.VAC) (SEQ ID NO: 126)

aligned with the nucleotide and deduced amino acid sequences of DEN-2 16681 virus (see SEQ ID NO:1). Dots in the DEN-1, DEN-3, and DEN-4 sequences signify identity with the DEN-2 sequence.

Figure 32: Partial amino acid sequences of candidate vaccine viruses:

DEN-1 16007 PDK-13	(D1.VAC) (SEQ ID NO: 124)
DEN-2 16681 PDK-53	(D2.VAC) (<u>see</u> SEQ ID NO: 2)
15. DEN-3 16562 PGMK-30/FRhL-3	(D3.VAC) (SEQ ID NO: 125)
DEN-4 1036 PDK-48	(D4.VAC) (SEQ ID NO: 126)

aligned with the deduced amino acid sequence of DEN-2 16681 virus (see SEQ ID NO:1). Dots in the DEN-1, DEN-3, and DEN-4 sequences signify identity with the DEN-2 sequence.

Figure 33: Mutagenesis analysis of the 5' end of the prM gene. The 447-452 sequence ("AACCAC" in DEN-2) can be mutated to "CTCGAG" in all four DEN viruses to create a XhoI site for cassette splicing. This modification results in conservative Thr-Thr to Ser-Ser substitutions at amino acid positions prM 4-5 in DEN-2 virus. By creating this XhoI site, all four viruses will contain the sequence FHLSSR at amino acid positions prM 1-6 (see Figure 32). Nucleotide mutations that are necessary to create the XhoI site are indicated by bold, underlined

characters in the nucleotide sequences of D2.VAC, D1.VAC, D3.VAC, and D4.VAC and their respective primers designed for amplification in PCR.

Figure 34: Mutagenesis analysis of the 3' end of the E gene. The 2344-2349 sequence ("TCACGC" in DEN-2) can be mutated to "TCTAGA" in all four DEN viruses to create a XbaI site for cassette splicing. This modification results in no amino acid change in DEN-2 at this site, but substitutions do occur in the other three viruses. By creating this XhoI site, all four viruses will contain the sequence SRS at amino acid positions E 470-472 (see Figure 32). Nucleotide mutations that are necessary to create the XbaI site are indicated by bold, underlined characters in the nucleotide sequences of D2.VAC, D1.VAC, D3.VAC, and D4.VAC and their respective primers designed for amplification in PCR.

Figure 35: Construction of DEN-2 PDK-53 cassette plasmids pF1-Xho and pF2-Xba. (A) pF1-Xho: Clone PCR cDNA amplicons F1-prM5' and F1-prM3' into TA-vector. Sequence and splice correct clones together at the SphI site in the TA-vector to construct pF1-prM53 (not shown). Subclone the prM53 cDNA into SstI/SphI-cut pF1-E (see Figure 20) to construct pF1-Xho. (B) pF2-Xba: Clone PCR cDNA amplicons F2-E5' and F2-E3' into TA-vector. Splice correct clones together at the XbaI site in the TA-vector to construct pF2-E53 (not shown). Subclone the SphI/HpaI E53 cDNA fragment into pF2-16B (see Figure 21), which itself is subcloned into pBRUC-139 between the SphI/KpnI sites (not shown), to construct pF2-Xho. PCR amplicon designations are underlined. Solid black bars indicate newly

synthesized and sequence-characterized cDNA. Stippled bar indicates previously synthesized cDNA. Graph resolution = 64.1857 nucleotides/dot.

Figure 36: Construction of chimeric plasmids

5 containing the prM and E genes (XhoI-XbaI cDNA fragment) of DEN-1, DEN-3, or DEN-4 candidate vaccine virus within the genetic background of DEN-2 PDK-53 virus. pD2V-CAS12 was constructed by ligating the SstI/SphI fragment of pF1-Xho and SphI/KpnI fragment of pF2-Xba (see Figure 33) into
10 a truncated form of pD2/IC-130V (see Figure 21). pD2/IC-130V was truncated by restricting the full-length clone at the NsiI-4696 and 3'-end XbaI sites, blunt-ending with T4 DNA polymerase, and religating. This procedure removed genome nucleotides 4696-10723, thereby removing the XhoI-
15 5426 and 3'-end XbaI sites, which would otherwise interfere with construction of chimeric plasmid cassettes using XhoI and XbaI sites. The cassette strategy employs PCR amplification of DEN-1, DEN-3, and DEN-4 cDNAs containing the prM and E genes; cutting the amplicons with
20 XhoI/XbaI; cloning resulting fragments into pD2V-CAS12 to construct pD1V-CAS12, pD3V-CAS12, and pD4V-CAS12 chimeric cassettes; confirming the chimeric XhoI/XbaI insert by nucleotide sequence analysis; and then subcloning the SstI/KpnI fragment of the chimeric cassette into pD2/IC-
25 130V to construct the chimeric full genome-length cDNA clones from which chimeric DEN-2/1, -2/3, and -2/4 viruses are derived. The genetic background of DEN-2 PDK-53 virus is illustrated by the solid black bars. The heterologous DEN-1, DEN-3, and DEN-4 cDNA inserts are indicated by the
30 stippled bars. The pBRUC-139 plasmid backbone is not

illustrated for pD1V-CAS12, pD3V-CAS12, or pD4V-CAS12 chimeric plasmid. Resolution = 110.5464 bp/dot.

Detailed Description of the Invention

5 We developed a quadravalent vaccine by initially constructing a full genome-length infectious cDNA clone for DEN-2 virus. We chose serotype 2 of DEN virus because virus strains of this serotype generally replicate to high titer in cell culture. We chose to develop an infectious
10 clone for the 16681 strain of DEN-2 virus because the candidate vaccine viruses developed by Mahidol University are currently the best live, attenuated vaccine virus candidates in terms of immunogenic efficacy and lack of reactogenicity in vaccinees. We developed an infectious
15 cDNA clone of the 16681 strain, which is the parent to the DEN-2 PDK-53 candidate vaccine virus developed at Mahidol University, to permit engineering of second and later generation live, attenuated DEN vaccine viruses.

The infectious clone strategy was initiated with the
20 virulent parental 16681 strain obtained from the Division of Vector-Borne Infectious Diseases (DVBID) of the Centers for Disease Control and Prevention (CDC) virus collection. We synthesized cDNA from the DEN-2 16681 viral RNA. The immediate objective was to obtain an accurate full genome-
25 length infectious cDNA clone of the 16681 strain of DEN-2 virus, since it was essential to develop a reliable experimental system to permit routine genetic engineering of the cDNA and recovery of virus. Our approach involved using polymerase chain reaction (PCR) technology to create
30 cDNA clones that could be spliced together to construct a

single full genome-length clone (Figure 1) from which full-length, infectious DEN-2 genomic mRNA could be transcribed (Figure 2).

The first full-length sequence-characterized cDNA clone, designated pD2/IC-20, was constructed in the high copy number pUC19 plasmid vector. Successful transcription of genome-length DEN-2 16681 viral RNA from pD2/IC-20 was clearly demonstrated by agarose gel electrophoresis of the transcription reaction product. However, RNA transcribed from this particular clone failed to yield infectious virus. It was determined that cDNA errors had occurred during the clone manipulations. We then decided to reconstruct the full-length clone in the low copy number pBR322 plasmid. The full-length cDNA of DEN-2 16681 virus was successfully moved into pBR322 to construct pD2/IC-30P. Full-length, infectious DEN-2 16681 genomic RNA was subsequently transcribed from pD2/IC-30P.

The DEN-1 PDK-13, DEN-2 PDK-53, DEN-3 PGMK-30/FRhL-3, and DEN-4 PDK-48 vaccine viruses were obtained from Mahidol University. Our goal involved replacement of the entire genomic cDNA backbone of the DEN-2 16681 full-length clone with the cognate cDNA cloned from the genome of the DEN-2 PDK-53 candidate vaccine virus. The prM and E genes of the DEN-2 PDK-53 virus are then replaced with the prM and E genes of the DEN-1 PDK-13, DEN-3 PGMK30/FRhL-3, and DEN-4 PDK-48 candidate vaccine viruses to construct chimeric DEN-2/1, DEN-2/3, and DEN-2/4 viruses containing the nonstructural genes of the DEN-2 PDK-53 virus and the prM and E genes of the heterologous DEN viruses.

DEN-2 PDK-53 Infectious cDNA Clone Backbone

	C		M		E		NS1		2A	2B		NS3		4A	4B		NS5		3'-NC
--	---	--	---	--	---	--	-----	--	----	----	--	-----	--	----	----	--	-----	--	-------

prM	E
-----	---

DEN-1 PDK-13

prM	E
-----	---

DEN-3 PGMK30/FRhL-3

prM	E
-----	---

DEN-4 PDK-48

It is contemplated that chimeric, infectious clone-derived DEN-2/1, DEN-2/3, and DEN-2/4 viruses will result in immediate improvement in the efficacy of a quadravalent vaccine. Our preliminary data from Mahidol University indicate that very small amounts of the DEN-2 PDK-53 vaccine virus were required to infect and immunize humans. However, the DEN-1, DEN-3, and DEN-4 vaccine virus candidates had approximately 30-fold to 2000-fold lower infectivity for humans. The low infective efficacies of the DEN-1, DEN-3, and DEN-4 viruses create significant problems in terms of vaccine efficacy in eliciting seroconversion in vaccinees, as well as problems of vaccine production for mass vaccination programs, since a large volume, up to 1 ml, of undiluted cell culture-derived vaccine virus must be administered to achieve even minimal levels of infectivity for these viruses. Since the increased infectivity of the DEN-2 PDK-53 vaccine virus is likely due to more efficient virus replication, and since this replicative efficacy is controlled by the nonstructural proteins of the virus, then chimeric vaccine viruses that express the relevant immunogenic structural proteins of DEN-1, DEN-3, or DEN-4 virus in the context of replication control by the nonstructural gene products of

the DEN-2 PDK-53 virus should replicate better and be more infective and immunogenic in human vaccinees than the original DEN-1, DEN-3, and DEN-4 vaccine viruses containing nonchimeric genotypes.

5

A quadravalent vaccine is obtained upon completion of the following steps:

- 10 (1) A full genome-length infectious cDNA clone for a DEN-2 virus, strain 16681, is constructed.
- 15 (2) A full genome-length infectious cDNA clone for a DEN2-16681 attenuated derivative, PDK-53, is constructed, preferably by substituting the genomic cDNA backbone of the DEN2-16681 full length clone with the corresponding cDNA cloned from the genome of the DEN-2 PDK-53 candidate vaccine virus.
- 20 (3) The candidate DEN-1, DEN-3, and DEN-4 vaccine viruses are subjected to PCR amplification of cDNA from extracted genomic RNA, and chimeric infectious cDNA clones expressing the prM and E genes of DEN-1, DEN-3, and DEN-4 viruses, respectively, in the context of the nonstructural genes of the DEN-2 PDK-53 virus are constructed.
- 25

(4) The infectious clone-derived chimeric DEN-2/1, DEN-2/3, and DEN-2/4 vaccine viruses are tested to ensure that they:

- 5 (a) Are viable;
- (b) Express appropriate virus-specific immunogens;
- (c) Replicate to sufficient titer in cell culture;
- 10 (d) Are infectious and immunogenic for humans; and
- (e) Retain phenotypic markers of attenuation.

There is no good animal model for investigating
15 dengue pathogenesis. DEN viruses are naturally transmitted between mosquitos and humans. Although lower primates can be infected with these viruses, they do not develop the clinical profiles that occur in humans. Infectious clone-derived viruses can be compared to their
20 more virulent parental strains using certain *in vitro* and *in vivo* markers:

In Vitro Markers:

- 25 Plaque size in cell culture;
- Temperature sensitivity;
- Cytopathic effects (CPE) in LLC-MK₂ cells; and
- Replication in macrophages.

In Vivo Markers:

- Virulence by intracranial route in mice;
- Viremia in monkeys;
- 5 Virulence by intracranial route in monkeys; and
- Elicitation of neutralizing antibodies in
- animals.

Infectious cDNA clones are expressed, the resulting
10 RNA transcripts are transfected into permissible cells,
and the live, attenuated viruses are formulated into
vaccines.

Additionally, the DEN-2 PDK-53 and chimeric DEN-
2/1, DEN-2/3, and DEN-2/4 infectious cDNA clones can by
15 themselves confer immunity by DNA immunization, a form of
gene therapy involving the direct inoculation of naked DNA
into the host such that its expression produces an immune
response (e.g., Ulmer et al., 1993 (DNA immunization
protected against influenza); Cox et al., 1993 (DNA
20 immunization protected against herpesvirus); Xiang et al.,
1994 (DNA immunization protected against rabies); Sedegah
et al., 1994 (DNA immunization protected against
malaria)).

Moreover, infectious cDNA clones are exquisite tools
25 for studying the molecular biology of virus structure,
function, and replication. This has been amply
demonstrated for many RNA viruses in the literature,
including Venezuelan equine encephalitis virus as reported
by Kinney et al. (1989). A successful infectious cDNA
30 clone of DEN-2 virus permits important investigations of

dengue virus replication, pathogenesis, and antigenic structure. Infectious clone cDNA templates permit the directed engineering of virus vaccines. Directed site-specific, nonrandom mutations can readily be made in
5 infectious cDNA clones, and therefore in clone-derived viruses, using a wide variety of DNA modification enzymes, restriction endonucleases, and *in vitro* mutagenesis methods. DNA is easier to manipulate than RNA, and the 10^{-9} error rate of DNA replication is much lower than the 10^{-3}
10 - 10^{-4} error rate produced by RNA polymerases. Infectious cDNA clones permit direct analyses of the phenotypic effects of individual and cumulative mutations in the viral genome. An infectious cDNA clone provides a "gold standard" reference sequence for a vaccine.

15

Particular aspects of the invention may be more readily understood by reference to the following examples, which are intended to exemplify the invention, without limiting its scope to the particular exemplified
20 embodiments.

EXAMPLESInformation:

Most of the background, protocols, and recipes used in recombinant DNA work can be found in *Molecular Cloning: A Laboratory Manual* (Sambrook et al., 1989), and *Current Protocols in Molecular Biology* (Ausubel et al., 1989).

Viruses:

The virulent parental DEN-2 16681 strain was immediately available in the DVBID collection of viruses. We received the DEN-1 PDK-13, DEN-2 PDK-53, DEN-3 PGMK-30/FRhL-3, and DEN-4 PDK-48 vaccine viruses from Mahidol University. The DEN vaccine viruses were passaged in primary dog kidney (PDK) cells because this cell culture is included among those cell types that are certified for human use by the Bureau of Biologics, US Food and Drug Administration (Yoksan et al., 1986). The virus strain designations are shown below:

	<u>Virus</u>	Parent <u>Strain</u>	Vaccine Derivative <u>Strain</u>
	DEN-1	16007	PDK-13
	DEN-2	16681	PDK-53
	DEN-3	16562	PGMK-30/FRhL-3

DEN-4

1036

PDK-48

PDK = primary dog kidney cells

FRhL = fetal rhesus lung cells

5 PGMK = primary green monkey kidney cells

DEN-1 16007 Parent

- ▶ Recovered from serum of a patient with hemorrhagic fever and shock in Thailand in 1964
- 10 ▶ Passaged 3X in BS-C-1 cells, 1X in LLC-MK₂ cells
- ▶ Passaged 2X in *Toxorhynchites amboinensis* mosquitos
- ▶ PDK-1

PDK-43 Vaccine

15

DEN-2 16681 Parent

- ▶ Recovered from serum of a patient with hemorrhagic fever and shock in Thailand in 1964
- ▶ Passaged 3X in BS-C-1 cells, 1X in LLC-MK₂ cells
- 20 ▶ Passaged 2X in *Toxorhynchites amboinensis* mosquitos
- ▶ PDK-1

PDK-53 Vaccine

25 DEN-3 16562 Parent

- ▶ Recovered from serum of a patient with hemorrhagic fever and shock in the Philippines in 1964
- ▶ Passaged 3X in BS-C-1 cells, 1X in LLC-MK₂ cells
- ▶ Passaged 2X in *Toxorhynchites amboinensis* mosquitos
- 30 ▶ PGMK-1

PGMK-30 DEN-3 virus grown in PGMK cells
↓
replicated to very low titer in
PDK FRhL-3 Vaccine cells (Yoksan et al., 1986)

5

DEN-4 1036 Parent

- ▶ Recovered from serum of a patient with dengue fever in Indonesia in 1976
- ▶ Passed 4X in *Aedes aegypti* mosquitos

10

▶ PDK-1

↓

PDK-48

The DEN-2 full-length cDNA clone was derived from the
15 DVBID seed of DEN-2 16681 virus, which had the passage
history:

Human

3X BS-C-1 cells

20

2X LLC-MK₂ cells2X *T. amboinensis* mosquitos4X C6/36 cells (*Aedes albopictus*)

Complementary DNA (cDNA) was amplified by RT/PCR
25 directly, without further cell culture passage, from virus
present in vaccine vials of the DEN-1 PDK-43, DEN-2 PDK-
53, DEN-3 PGMK-30/FRhL-3, and DEN-4 PDK-48 viruses..

Stock virus seed was prepared from virus-infected
cells grown in 75 or 150 cm² plastic tissue culture flasks.

30 The culture medium was clarified by centrifugation for 30

min at 10,000 rpm in a Sorvall GSA rotor, bringing the final concentration of fetal bovine serum (FBS) to 10% (v/v), and then freezing the clarified virus suspension in aliquots of 0.5 - 1.0 ml at -70°C. Gradient purified DEN-
5 2 16681 virus was prepared according to the method of Obijeski et al. (1976) as reported by Kinney et al. (1983).

Cell Lines:

10

Infectious virus was derived from the infectious cDNA clones by electroporation of BHK-21-15 (baby hamster kidney-21, clone 15) cells with transcribed viral RNA. Viruses were also grown in LLC-MK₂ monkey kidney cells,
15 Vero African green monkey kidney cells, and C6/36 mosquito cells (*Aedes albopictus* C6 cells, clone 36, Igarashi (1978)). All four cell lines were grown in Eagle's minimal essential medium (MEM) supplemented with 10% (v/v) heat-inactivated (56°C for 30 min) FBS, 1.25 g/L of sodium
20 bicarbonate, 100 units/ml of penicillin G, and 100 µg/ml of streptomycin sulfate. Confluent cell monolayers grown in plastic tissue culture flasks were infected by decanting the growth medium, permitting the virus inoculum to adsorb for 1.5 h at 37°C, and then adding MEM
25 containing 5% FBS. For plaque titration of viruses, confluent cell monolayers in plastic 6-well trays were inoculated with 200 µl of the appropriate dilution of virus. Virus was adsorbed to the cell monolayer for 1.5 h at 37 °C. The cells were then overlaid with 3 ml of 1%
30 (w/v) Noble agar (maintained at 40°C) in MEM lacking

- phenol red pH indicator and containing 2% FBS and 0.01% (w/v) DEAE-dextran. Following incubation for 6 days at 37 °C in a 5% CO₂ atmosphere, a second 1-ml agar overlay containing 50 µg/ml of neutral red vital stain was added.
- 5 Viral plaques were counted 2-5 days later.

E. coli:

- The *E. coli* K-12 strains used in this project
- 10 included XL1-Blue, MC-1061, SURE, JM101, and TB-1. Recombinant plasmid containing full genome-length cDNA of DEN-2 virus was successfully replicated in *E. coli* XL1-Blue, MC-1061, and TB-1. Flavivirus cDNA, particularly the gene region encoding the envelope glycoprotein, is
- 15 troublesome in *E. coli*. Bacteria hosting the recombinant plasmid containing the full-length cDNA clone grew slowly and were often difficult to streak for isolation on agar plates containing selective antibiotic. Transformation efficiencies were sometimes improved somewhat by
- 20 incubation of agar plates at 30°C or ambient temperature rather than at 37°C. Bacterial stocks were stored frozen at -70°C in 10% (v/v) glycerol.

Precautions for Working with RNA:

25

- RNA is a fragile molecule that is very readily degraded by the many ubiquitous RNases present in the environment. Many of these RNases are resistant to treatment with detergents and heat, including autoclaving.
- 30 All reagents and materials that contacted the viral RNA in

this project were RNase-free to avoid degradation of the viral RNA by these ubiquitous, very stable enzymes. The investigator wore tight-fitting gloves, maintained all reagents on ice, used a plastic tool to open the lids of microtubes, used individually packaged pipets, preferably plastic for aqueous solutions, disposable plasticware which is generally RNase-free before opening, and used "For RNA Only" microtubes, Gilson micropipetors (P-10, P-20, P-100, P-200, P-1000) and tips with aerosol barriers. Use of recycled glassware was avoided. Weigh boats, magnetic stirrers, and pH meters were not used. Chemicals were weighed in sterile, RNase-free disposable plastic 50-ml centrifuge tubes, and solutions were adjusted to the appropriate pH by aliquoting a small volume of the solution onto pH paper. Whenever possible, commercially prepared, guaranteed RNase-free reagents were purchased. Otherwise, newly-opened chemicals were reserved "For RNA Only". Water and stock salt solutions, except for those containing Tris, were treated overnight with 0.1% (v/v) diethylpyrocarbonate (DEPC) to inactivate RNases via alkylation and then autoclaved for 20 min. It is advisable to use the best sterile technique when working with RNA.

25 Extraction of Viral Genomic RNA from Virus Seed:

Virus seeds containing at least 10^6 PFU (plaque forming units)/ml of virus are ideal for providing appropriate yields of RNA. Seed with virus titer of 10^4 or lower can be problematic in terms of yielding sufficient

RNA. For these low-titer seeds it is best to pool the yields of several extracted seed aliquots.

RNA extraction involved the addition of 200 μ l of cold RNA lysis buffer (4 M guanidine isothiocyanate, 25 mM sodium citrate, pH 7.0, 0.5% (w/v) sarkosyl, and 100 mM beta-mercaptoethanol), and 30 μ l of 3 M sodium acetate, pH 5.2, to an empty RNase-free 1.5-ml microtube on ice. In a biosafety cabinet, 200 μ l of DEN virus seed was added to the microtube and mixed vigorously for 30 sec with a mechanical mixer. The tube was centrifuged briefly to pellet the liquid; then 400 μ l of cold phenol (commercially supplied by AMRESCO) equilibrated to pH 4.5 and 80 μ l of cold chloroform were added. The tube was mixed vigorously for 30 sec, placed on ice for 15 min, mixed again, then centrifuged for 1 min at maximum speed in a refrigerated microcentrifuge to separate the aqueous and organic phases. The top aqueous phase containing the extracted RNA was transferred to a fresh 1.5-ml microtube on ice, 400 μ l of cold isopropanol was added, and the tube was incubated for at least 1 h or overnight at -20°C. The RNA was precipitated by centrifugation for 10 min at maximum speed at 4°C. The supernatant was removed with a pipet rather than by decantation and rinsed with 500 μ l of 75% (v/v) ethanol. After spinning again for 10 min, the ethanol was removed with a pipet. The tube was centrifuged again briefly and the residual liquid was removed with a micropipet. The RNA pellet was air dried briefly, resuspended in 50 μ l of cold RNase-free dH₂O, and stored frozen. For seeds containing low virus titer, the

RNA pellets in 3-6 microtubes were pooled in a total volume of 50 μ l.

RT/PCR Synthesis of Dengue Virus-Specific cDNA Fragments

5

Full-length genomic mRNA was extracted directly from 200 μ l of DEN virus seed. The standard reverse transcriptase/polymerase chain reaction (RT/PCR) was performed in a 100- μ l reaction solution containing 5-18 μ l of the extracted viral RNA, 1 μ l each of 100 μ M stock solutions (stored frozen in dH_2O) of the upstream mRNA-sense primer-amplimer and downstream complementary-sense primer-amplimer, 10 μ l of 10X standard PCR buffer (500 mM KCl, 100 mM Tris-HCl, pH 8.5, 15 mM MgCl_2 and 0.1% (w/v) gelatin), 8.0 μ l of 2.5 mM dNTPS (2.5 mM each of dATP, dCTP, dGTP, and dTTP; Pharmacia-LKB), 0.5 μ l of 1 M dithiothreitol (DTT), 0.5 μ l of RNase inhibitor (RNasin, 40 U/ μ l, Boehringer-Mannheim), 0.5 μ l of Taq DNA polymerase (5 U/ μ l, Perkin-Elmer), and 0.5 μ l of RAV-2 reverse transcriptase (18 U/ μ l, Takara). The reaction solution was made as two components:

10

15

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38

5	PCR Reaction Mix:	10.0 μ l	10X Standard PCR Buffer
		8.0 μ l	2.5 mM dNTPs
		0.5 μ l	1 M DTT
		0.5 μ l	RNasin (40 U/ μ l)
		0.5 μ l	Taq DNA Polymerase (5 U/ μ l)
		0.5 μ l	RAV-2 RT (18 U/ μ l)
		<u>60.0 μl</u>	<u>RNase-Free dH₂O</u>
10		80.0 μ l	Reaction Mix for 1 reaction. Make more than needed for all reaction tubes. Store excess at -70°C for reuse.
15	Template/Primer Mix:	18.0 μ l	DEN-2 RNA Template
		1.0 μ l	100 μ M Up-Amplimer
		<u>1.0 μl</u>	<u>100 μM Down-Amplimer</u>
		20.0 μ l	
20	Reaction Solution:	80.0 μ l	PCR Reaction Mix
		<u>20.0 μl</u>	<u>Template/Primer Mix</u>
		100.0 μ l	In a thin-walled, 200- μ l microtube.

25

The RT/PCR reactions in thin-wall 200- μ l microtubes (Phenix Research Products) were incubated without oil overlay in a Perkin-Elmer Model 9600 thermocycler according to the following program:

30

35

40

50 °C for 60 min = First strand cDNA synthesis
by reverse transcriptase

94°C for 4 min

50°C for 1 min

72°C for 5 min

94°C for 30 sec

55°C for 30 sec

72°C for 5 min

Delta +10 sec/cycle

30 Cycles

Following completion of the RT/PCR reactions, 5- μ l aliquots of each of the 100- μ l reactions were analyzed by agarose gel electrophoresis. The DNA bands in the agarose gel were stained in ethidium bromide (500 ng/ml) solution and visualized on an ultraviolet light box. Since extraneous non-target cDNA bands are often amplified in addition to the target cDNA molecules, the remaining 95 μ l of each RT/PCR reaction was electrophoresed in a larger, preparative agarose gel, and the target cDNA was stained briefly, excised with a razor blade, and physically extracted from the agarose slice.

High-Melt-Crush (HMC) Extraction of DNA from Agarose:

An agarose gel slice containing DNA was placed in a 1.5-ml microtube and crushed thoroughly with a spatula or pestle. The volume of the crushed agarose was brought to 400-500 μ l with TE buffer (10 mM Tris-HCl, pH 7.5, 1 mM disodium EDTA) and 400 μ l of phenol (supplied by AMRESCO), pH 8, was added. The agarose suspension was mixed vigorously using a mechanical mixer, frozen, thawed and mixed, frozen, thawed and mixed, and then centrifuged for 10 min at maximum speed at 4°C. The top aqueous phase was transferred to a fresh microtube, extracted with 400 μ l of phenol:chloroform:isoamyl alcohol (25:24:1) and centrifuged for 2 min. The top aqueous phase was transferred to a fresh tube and extracted with 700 μ l of diethyl ether or chloroform. If chloroform was used, the top phase was again transferred to a fresh tube after a brief spin to separate phases. The DNA was precipitated

for at least 30 min at -70°C or overnight at -20°C following addition of 2.5 volumes (essentially filling the microtube) of 95% ethanol containing 300 mM ammonium acetate and 10 mM MgCl₂. The DNA was pelleted at 4°C by centrifugation for 20 min at maximum speed. The liquid was decanted, and the DNA pellet was rinsed with 500 µl of 75% ethanol, air-dried briefly, dissolved in 30 µl of TE buffer, and stored frozen or in the refrigerator. A 3-µl aliquot of the extracted DNA was analyzed for purity and quantity by agarose gel electrophoresis. Generally, 20-80% of the DNA loaded onto a gel can be recovered from the gel by this method.

Agarose Gels:

15

DNA was analyzed by electrophoresis in 1% (w/v) agarose gels run in TBE buffer (100 mM Tris-HCl, pH 8, 91 mM boric acid, and 20 mM disodium EDTA). DNA bands were visualized by staining the gel in water containing 500 ng/ml of ethidium bromide and exposure to ultraviolet light. Gels used for analyzing RNA transcripts were made with RNase-free reagents. Ethidium bromide stain was incorporated in the gel and running buffer so that the RNA bands could be visualized immediately. To obtain gel-purified DNA fragments, DNA was electrophoresed in 0.7% (w/v) agarose gels made with genetic technology grade Seakem agarose (FMC) or with biotechnology grade agarose (3:1 high resolution blend, AMRESCO).

Cloning of Dengue Virus-Specific cDNA Fragments:

Some DNA polymerases add an extra "A" nucleotide
5 overhang at the 3'-end of synthesized DNA strands. The
Taq DNA polymerase does this. To enable the cloning of
DNA molecules synthesized using Taq DNA polymerase, TA-
cloning vectors have been engineered (Marchuk et al.,
1991). These vectors generally have a single "T" overhang
10 engineered at the 3'-terminus of EcoRV-cut, blunt-ended,
linearized plasmid vector. The EcoRV site occurs within
the multiple cloning site (MCS) of the plasmid. The MCS
is a series of contiguous, unique restriction enzyme
(REnz) sites engineered into a vector plasmid to permit
15 - subcloning of exogenous DNA fragments following
restriction with a variety of RENZs. The HMC-purified DEN
cDNA amplicons were cloned into the 3900-bp pCRII
(Invitrogen), the 2887-bp pT7Blue(R) (pT7Blue, Novagen),
or the 3003-bp pGEM-5Zf (Promega) TA-vector plasmid. The
20 RENZ sites available in the MCS region of these TA-
vectors, as well as the RENZ sites of the MCS of the
general purpose cloning plasmids, pUC18 and pUC19, used in
this project are shown below.

RENZ Sites Present in the MCS of Several Cloning Vectors

	<u>pUC18</u>	<u>pUC19</u>	<u>pT7Blue</u>	<u>pCRII</u>	<u>pGEM-5Zf</u>
5			T7	SP6	T7
	EcoRI	HindIII	HindIII	NsiI	ApaI
	SstI	SphI	BspMI	HindIII	AatII
	KpnI	PstI	SphI	KpnI	SphI
10	SmaI	SalI	PstI	SstI	NcoI
	BamHI	XbaI	Sse8387I	BamHI	SstII
	XbaI	BamHI	SalI	SpeI	<u>EcoRV</u>
	SalI	SmaI	AccI	BstXI	SpeI
	PstI	KpnI	HincII	EcoRI	NotI
15	SphI	SstI	XbaI	<u>EcoRV</u>	PstI
	HindIII	EcoRI	SpeI	EcoRI	SalI
			NdeI	PstI	NdeI
			<u>EcoRV</u>	BstXI	SacI
			BamHI	NotI	BstXI
20			AvaI	AvaI	NsiI
			SmaI	SphI	SP6
			KpnI	NsiI	
			SacI	XbaI	
			BanII	ApaI	
25			EcoRI	T7	

The pUC18/19 plasmids possess identical MCS sites in reverse orientation in the plasmid backbone. Their purpose is to permit cloning of DNA in either orientation into the plasmid using the same pair of RENZs - this

reversibility was exploited in this project. The TA-vectors used here all possessed T7 and/or SP6 bacteriophage RNA promoters to enable RNA transcription from cloned DNA. These promoters were not used in this project. All of the plasmids contain the gene for ampicillin resistance. They also contained the *lac Z* portion of the *E. coli lac* operon. This permits color discrimination between bacterial colonies that receive a recombinant or a wild-type plasmid. In the presence of IPTG and X-gal, bacterial colonies that are transformed with a wild-type plasmid lacking a cDNA insert develop a blue color, whereas cells that receive a recombinant plasmid with cDNA cloned into the MCS of the plasmid are white. Agar plates contained 800 μ g of IPTG and 800 μ g of X-gal.

Fifty to 100 ng of HMC-purified amplicon was ligated to 50 ng of the pCRII vector using the TA-vector cloning kit supplied by Invitrogen exactly as specified by the instructions supplied with the kit. Frozen, transformation competent *E. coli* INV α F' cells, supplied with the Invitrogen kit and stored at -70°C, were transformed with the ligated DNA as described in the kit instructions. The transformed cells were plated on YTA₅₀ agar plates (8 g of DIFCO tryptone, 5 g of DIFCO yeast extract, 5 g of NaCl, and 15 g of BACTO agar per liter of dH₂O) containing 50 μ g/ml of ampicillin. Only bacterial cells transformed with the pCRII plasmid, which contains an ampicillin resistance gene, grow on this medium. The agar plates were incubated at 37°C overnight.

Similarly, cDNA was ligated to the other TA-vectors or to pUC18/19 cut with the appropriate RENZ(s). Ligations were performed at room temperature or at 12°C. *E. coli* XL1-Blue, SURE, TB-1, or MC-1061 cells were transformed by electroporation and plated on YTA₅₀ plates. Electroporation was performed according to Dower et al. (1988) using cuvettes with a 2-cm electrode gap in a Bio-Rad Gene Pulser set at 2.5 kV voltage, 25 μ F capacitance, and 200 ohms resistance. Electroporation-competent cells were prepared by growing a fresh bacterial culture to an optical density of 0.5-0.7 at 600 nm. The cells from 1.5 - 3 L of culture were pelleted by centrifugation for 10 min at 4°C and 5000 rpm in a Sorvall GSA rotor, pooled, washed twice in 1 mM Hepes buffer, and resuspended in 2 ml of 10% (v/v) sterile glycerol per L of original culture. The concentrated cells in glycerol were stored at -70°C.

Bacterial colonies were transferred to 2 ml of 2XYT-Amp₅₀ broth (16 g of tryptone, 20 g of yeast extract, and 5 g of NaCl per liter of dH₂O) and incubated overnight with shaking at 300 rpm at 37°C in a floor model incubator - shaker (model Innova 4300, New Brunswick). Recombinant plasmid was extracted from these 2-ml minicultures and analyzed by agarose gel electrophoresis for the presence of cDNA insert. Recombinant plasmids are larger than wild type vector plasmid because of the cDNA insert, and they migrate more slowly than wild type plasmid in agarose gels.

All of the DEN-2 16681 virus-specific cDNA amplicons were cloned into the pCRII TA-vector. Aliquots of insert-positive miniprep plasmids were digested with the

restriction enzyme EcoRI. Since the pCRII MCS contains two EcoRI recognition sites (palindromic hexameric sequence GAATTC) on either side of the EcoRV cDNA cloning site, this RENZ cleaved the cDNA insert from the plasmid vector and cleaved any EcoRI sites that were present within the cDNA itself. The EcoRI-restricted DNA was analyzed by agarose gel electrophoresis to determine that the cloned cDNA was of appropriate size. In our experience, cloning of PCR-derived cDNA amplicons 2000 bp or smaller in size into the TA-vector is efficient. Cloning amplicons larger than 3500 bp into the TA-vector can be very difficult.

After screening, certain of the miniprep plasmids were selected for further analysis. Their corresponding bacterial minicultures were streaked for isolation on YTA₅₀ plates, and an isolated colony was inoculated into 50-200 ml of YTA₅₀ broth to grow up a preparative amount of recombinant plasmid. The preparative scale for the extraction of the plasmid was essentially identical to that for minipreps except for scaled up volumes.

Extraction of Plasmid DNA from Minicultures of *E. coli*:

White colonies containing recombinant plasmid were picked with a sterile toothpick and shaken overnight at 300 rpm in 2 ml of 2X-YTA₅₀ broth. Each miniculture was decanted into a 1.5-ml microtube, and the cells were pelleted by centrifugation at 6000 rpm for 2 min. The supernatant was aspirated, and the cell pellet was resuspended gently by up/down micropipeting in 200 μ l of

GTE buffer (50 mM glucose, 25 mM Tris-HCl, pH 8.0, and 25 mM disodium EDTA) and then mixed with 300 μ l of lysis buffer (0.2 N NaOH, 1% (w/v) sodium dodecylsulfate (SDS)). After incubation on ice for 5 min, 300 μ l of cold
5 potassium acetate solution (3 M potassium acetate, 7 M acetic acid, pH 4.8) was added, and the solution was chilled for 5 min on ice and then centrifuged at maximum speed for 10 min at 4°C. The supernatant was poured into a fresh microtube, RNase A was added to 20 μ g/ml, and the
10 mixture was incubated at 37°C for 30 min. The sample was extracted twice with 600 μ l of chloroform and centrifuged for 1 min at maximum speed at room temperature. The DNA pellet was dissolved in 32 μ l of dH₂O. Eight μ l of 4M NaCl and 40 μ l of 13% (w/v) PEG-8000 was added, and the mixed
15 solution was incubated for 5 min on ice. The sample was centrifuged for 15 min at maximum speed at 4°C, the liquid was aspirated with a micropipet, and the pellet was rinsed with 500 μ l of 75% ethanol. The air dried pellet was dissolved in 30 μ l of dH₂O and stored frozen until
20 used.

Extraction of Plasmid DNA from Large Cultures of *E. coli*:

Preparative-scale plasmid extraction was performed by
25 inoculating 100 ml of 2X-YTA₅₀ broth with 2 ml of an overnight culture of *E. coli*. The culture was shaken overnight at 300 rpm and 37°C. The cells were pelleted by centrifugation for 10 min at 5000 rpm in a Sorvall GSA rotor and resuspended in 6 ml of cold GTE buffer. Nine ml
30 of a freshly made solution of 0.2 N NaOH and 1% (w/v) SDS

was added. The sample was incubated for 5 min on ice, then 9 ml of cold 3 M potassium acetate solution was added. After another 5-min incubation on ice, the tube was centrifuged for 20 min at 10,000 rpm at room temperature and the supernatant was transferred to a fresh 30-ml glass tube. RNase A was added to 20 μ g/ml, and the sample was incubated for 30 min at 37°C and then extracted twice with 6 ml of chloroform. Twelve ml of room-temperature isopropanol was added and the tube was centrifuged immediately for 20 min at 10,000 rpm at room temperature. The supernatant was decanted, and the DNA pellet was rinsed with 1 ml of 75% ethanol, air dried briefly, and resuspended in 480 μ l of dH₂O. The DNA was precipitated by addition of 120 μ l of 4 M NaCl and 600 μ l of 13% PEG-8000, incubation for 5 min on ice, and centrifugation for 15 min at maximum speed at 4°C. The DNA pellet was rinsed with 500 μ l of 75% ethanol, air dried briefly, rehydrated in TE buffer, and stored frozen.

20 Nucleotide Sequence Analysis of the Dengue cDNA Clones:

Nucleotide sequence analyses of DEN-2 16681 cDNA clones #1-#15 were performed by cloning EcoRI restriction fragments of each clone into the single-stranded bacteriophage M13mp18 or M13mp19. Since this is not the current method of choice for sequencing, the method will be described only briefly here. The procedure used for the extraction of plasmid DNA from bacterial cells was also used to extract the intracellular double-stranded replicative form (RF) DNA of M13 from bacteriophage-

infected *E. coli* JM101 cells. The RF DNA was linearized at the EcoRI site of the MCS and ligated to the DEN-2 HMC-purified EcoRI cDNA restriction fragments.

Electroporation-competent *E. coli* JM101 cells were transformed by electroporation and plated onto H-agar plates (10 g of DIFCO tryptone, 5 g of NaCl, 15 g of BACTO agar, and 1% (w/v) thiamine per liter of dH₂O) containing 800 µg each of isopropyl-β-D-galactopyranoside (IPTG) and 5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside (BCIG or X-gal). The electroporated cells were mixed with 300 µl of a fresh logarithmic culture of JM101 cells and 3 ml of warm (51°C) top H-agar containing 9 g/L of agar and then poured onto the H-agar plates. Cells that were transfected with recombinant DNA supported replication of recombinant M13 virus, resulting in the formation of bacteriophage plaques in the JM101 cell lawn on the agar plate. The IPTG/BCIG histochemistry of the system permitted identification of white plaques containing recombinant bacteriophage into which cDNA had been ligated into the EcoRI site of the MCS, whereas wild-type nonrecombinant M13 bacteriophage produced blue plaques. Isolated plaques were picked, inoculated into 3 ml of a fresh, pre-logarithmic phase culture of JM101, and shaken at 37°C for 8-16 h. The minicultures were clarified by centrifugation in 1.5-ml microtubes, the bacteriophage particles were precipitated with PEG-8000, and the single-stranded, circular bacteriophage DNA was isolated from the virions by phenol extraction. The recombinant, circular, single-stranded bacteriophage DNA was sequenced by the dideoxynucleotide termination method. Sequencing kits can

be purchased from various commercial vendors. Radioactive ^{32}P -dCTP or ^{35}S -dCTP was incorporated into the strands synthesized in the sequencing reactions. Sequencing was accomplished with many DEN-2 virus-specific primers
5 designed to sequence the entire genome. The sequence reactions were electro-phoresed in 6% (w/v) polyacrylamide gels, which were dried onto filter paper and overlaid with X-ray film. The DNA bands of the autoradiographs were read by the investigator, and the data was entered into a
10 sequence project data spreadsheet. This sequencing method has been used extensively in the past (e.g., Kinney et al., 1986; Johnson et al., 1986; Deubel et al., 1986; Deubel et al., 1988; Kinney et al., 1989; Trent et al., 1987).

15 Nucleotide sequencing was also performed by the current method of direct sequencing of double-stranded plasmid DNA by the dideoxynucleotide termination method using the Applied Biosystems Taq DyeDeoxy Terminator Cycle Sequencing Kit, cycle sequencing in the Model 9600
20 thermocycler according to the instruction manual supplied with the kit, and analyzing the DNA sequence on an ABI Model 373A DNA sequencing apparatus. Sequencing reactions in 200- μl thin-walled microtubes contained 9.5 μl of reaction mix (buffer, the four dideoxynucleotides, and Taq
25 polymerase supplied in the kit), 7.0 μl of double or single-stranded template DNA (150 pg/bp), and 3.2 μl of 10 μM sequencing primer (32 pmol). After mixing, the reactions were placed in a Perkin-Elmer Model 9600 thermocycler, and programmed cycle sequencing was
30 performed for 25 cycles of incubation at 96°C for 15 sec,

50

50°C for 15 sec, and 60°C for 4 min. Strand extension was performed at 60°C rather than 72°C because the fluorescent dye-labeled dideoxynucleotide terminators are heat sensitive. The reaction was then applied to a Centrisep gel column (Princeton Separations) to remove unincorporated dye-labeled dideoxynucleotides according to the instructions supplied with the columns. The eluted DNA was vacuum dried for 1 h using a Savant Speed Vac Concentrator and stored at -70°C. The DNA was hydrated with 5 μ l of deionized formamide and 1 μ l of 50 mM disodium EDTA, then heated in an aluminum block for 2 min at 90°C. A 3- μ l aliquot of the denatured DNA sample was applied to one of 24 wells of a polyacrylamide-urea gel in an Applied Biosystems 373A DNA sequencer. The color-coded sequence chromatograph was read by visual inspection, and the resulting nucleotide sequence was entered into a computer-maintained sequence data spreadsheet. The sequencing kit incorporates dideoxynucleotide terminators that are each labeled with a unique fluorescent dye that permits laser detection of all four terminators in a single polyacrylamide gel lane in the Model 373 sequencer. The data was recorded in the form of colored chromatograms that are easily read by the investigator. Single-stranded recombinant M13 DNA can also be sequenced in this manner.

Extraction of M13 Single-Stranded DNA for Sequencing:

White bacteriophage plaques containing recombinant M13 DNA were picked with sterile toothpicks and placed into 2-ml slightly turbid (less than 0.15 A_{600}) cultures of

E. coli JM101. The cultures were shaken at 300 rpm and 37°C overnight and then clarified by centrifugation in microtubes at maximum speed for 10 min at room temperature. One ml of the supernatant was transferred to a fresh 1.5-ml microtube containing 200 µl of sterile 20% (w/v) PEG-8000 in 250 mM NaCl. The tubes were mixed by inversion, incubated for 15 min at room temperature, and centrifuged at maximum speed for 5 min at room temperature. The PEG supernatant was removed completely, and the DNA pellet was resuspended in 300 µl of TE buffer. An equal volume of pH 8-buffered phenol was added, and the solution was mixed vigorously several times during a period of 20 min at room-temperature. The tube was centrifuged for 5 min at room temperature, and the top aqueous phase was transferred to a fresh 1.5-ml microtube. After sequential extraction with phenol:chloroform:isoamyl alcohol and chloroform, the DNA was precipitated by adding 2.5 volumes of 95% ethanol containing 300 mM ammonium acetate and 10 mM MgCl₂, and incubating at -20°C overnight. The tube was centrifuged at maximum speed for 15 min at 4°C, and the supernatant was decanted. Following a rinse with 500 µl of 75% ethanol, the DNA was air dried briefly, resuspended in 60 µl of TE buffer, and stored at 4°C.

25 Primers:

Primer design was based on the sequence of DEN-2 virus, strain 16681, published by Blok et al. (1992), and DEN-2 virus, Jamaican strain 1409, as reported by Deubel et al. (1986) and Deubel et al. (1988).

Primers were synthesized by the Biotechnology Core Facility at the CDC in Atlanta, Georgia. We received the dried primers via mail and adjusted them to a concentration of 100 μ M in dH₂O. The designations and sequences of all of the primers-amplimers used in this project are listed in Appendix A.

To amplify the 3'-end of the DEN-2 virus genome, a downstream amplimer was designed that was complementary to the published sequence of the 3' terminus of the genome. A unique XbaI restriction enzyme site was incorporated at the 5' end of this amplimer to provide a unique site to permit linearization of the recombinant plasmid containing the full-length cDNA clone at the 3' terminus of the cloned genomic cDNA. This linearization was necessary to obtain appropriately terminated DEN virus-specific run-off RNA transcripts from the cDNA clone in transcription reactions with bacteriophage T7 RNA polymerase. Linearization at this 3'-terminal XbaI site resulted in the incorporation of a 5-nucleotide TCTAG extension to the 3' terminus of the genomic mRNA transcribed from the full-length cDNA clone of DEN-2 16681 virus, and a 4-nucleotide CTAG extension to the 3' terminus of RNA transcribed from the DEN-2 PDK-53 cDNA clone. The difference between the two cDNA clones in the length of the extraneous 3'-terminal extension was due to the differently designed 3'-terminal amplimers used to obtain the 3' end genomic cDNA amplicon. Amplimer cD2-10687.XBA or cD2-10687.X2 was used to amplify and clone the 3'-terminal portion of DEN-2 16681 or PDK-53 virus, respectively.

The promoter for the bacteriophage T7 RNA polymerase was engineered at the 5' terminus of the cloned genomic cDNA by incorporating the recognition sequence of the T7 RNA polymerase into the sequence of the 5'-terminal upstream, mRNA-sense amplicon D2-SMT71 immediately preceding the 5'-terminal nucleotide of the DEN-2 viral genome. This design ensured that the T7 RNA polymerase initiated RNA transcription at the 5'-terminal nucleotide of the DEN-2 virus-specific cDNA (Milligan et al., 1987).

Amplimers for PCR reactions were designed to take advantage of RENZ sites identified within the nucleotide sequence of the genome of DEN-2 16681 virus. cDNA molecules were amplified to permit ligation or splicing together of overlapping contiguous cDNA clones at shared, overlapping, unique RENZ sites (Figure 3).

Transcription of Genomic mRNA from DEN Virus-Specific Full-Length cDNA Clones:

The recombinant plasmid containing the full-length cDNA clone was prepared for RNA transcription by linearization at the unique XbaI site located at the 3' terminus of the cloned genomic cDNA. The restriction reaction containing the XbaI-restricted plasmid was extracted sequentially with phenol:chloroform:isoamyl alcohol and chloroform and then precipitated. The DNA was redissolved in 50 μ l of TE buffer and digested with proteinase K at a concentration of 1 mg/ml for 1 h at 37°C to hydrolyze contaminating RNases. The sample was then extracted twice with "For RNA Only" phenol:chloroform:isoamyl alcohol buffered to pH 8,

extracted twice with chloroform to remove traces of phenol, and precipitated by adding one-tenth volume of RNase-free 3 M sodium acetate, pH 5.2, and 2.5 volumes of ethanol and incubating for at least 1 h at -70°C or
5 overnight at -20°C.

DEN-2 virus-specific genomic RNA was transcribed from the linearized cDNA template using a commercial T7 transcription kit (Ampliscribe T7 transcription kit, Epicentre Technologies). Transcription reactions were
10 performed for 2 h at 37°C in RNase-free 1.5-ml microtubes in 20- μ l reactions containing 100-1000 ng of linearized DNA template, 7.5 mM each of CTP, GTP, and UTP, 0.75 mM ATP, 2.7 mM m⁷GpppA cap analog, 6.7 mM DTT, 2.0 μ l of a 10X concentration of a proprietary buffer supplied with
15 the commercial kit, and 2.0 μ l of the proprietary Ampliscribe enzyme solution supplied with the kit. Reaction solutions were used directly and without further treatment to transfect BHK-21 cells.

20 Transfection of BHK-21 Cells with Genomic RNA Transcripts:

BHK-21 clone 15 cells were transfected with RNA transcripts by electroporation (Liljeström et al., 1991). Fresh cultures of BHK-21 cells were grown to 90%
25 confluency, rinsed twice with cold RNase-free phosphate buffered saline (PBS), and released from the plastic by incubation with 3 ml of commercial trypsin-EDTA solution (GIBCO-BRL). The cells were pelleted by low-speed centrifugation at 1200 rpm for 5 min in a Beckman GPKR
30 centrifuge. The cells were washed twice with cold PBS,

resuspended in cold PBS and kept on ice. The cells were counted using a hemacytometer and microscope, and the cell concentration was adjusted to 10^7 cells/ml. One-half ml of the washed, adjusted cells were mixed with each
5 transcription reaction solution in 1.5-ml microtubes on ice. The mixture was transferred to a cold electroporation cuvette with 0.2-cm electrode gap, which was placed in the cuvette holder of the Bio-Rad Gene Pulser. The cells were shocked twice using settings of
10 1.5 kV voltage, 25 μ FD of capacitance, and resistance set to infinity. The shocked cells were incubated for 10 min at room temperature and then added to 75 cm² tissue flasks containing 20 ml of MEM containing 10% FBS. Transfected cell cultures were incubated at 37°C for 5-8 days until
15 CPE was evident in the cell monolayer and/or expression of DEN virus-specific antigens was identified in an aliquot of the cell monolayer scraped from the flask using DEN virus-specific mouse hyperimmune ascitic fluid or monoclonal antibodies in indirect immunofluorescence
20 tests.

RESULTS

Replication of DEN-2 16681 Virus:

25 DEN-2 16681 virus replicates to high titer in cell culture. The CDC virus seed used in this study contained 2.0×10^7 plaque forming units (PFU)/ml. This titer was determined by plaque titration of the seed virus in monolayer cultures of Vero cells. This seed titered $1.3 \times$
30 10^4 PFU/ml in LLC-MK₂ cells. A growth curve for this virus

was determined in C6/36 *Aedes albopictus* cell culture (Figure 4). This level of replication is quite high for a flavivirus. The DEN-2 16681 virus is eminently suitable to serve as the parent to an infectious cDNA clone of DEN virus.

The DEN-2 PDK-53 vaccine virus, taken directly from a vaccine vial obtained from Mahidol University, contained 3.4×10^4 PFU/ml of virus, as titrated in Vero cell monolayers, and 1.5×10^4 PFU/ml as titrated in LLC-MK₂ cell monolayers.

RT/PCR Amplification and Cloning of DEN-2 16681 cDNA:

The entire genome of DEN-2 virus, parental strain 16681, was amplified from genomic RNA in the form of 5 cDNA clones of various sizes (T7-F1, F2, F3, F4, and F5). PCR amplification with 5 sets of upstream and downstream amplimers yielded the predicted amplicon sizes in PCR reactions. Figure 5 shows the migration of these cDNA fragments in agarose gels.

Recombinant plasmids, obtained by ligating the cDNA amplicons into the pCRII TA-vector, were extracted from minicultures derived from transformed *E. coli* XL1-Blue colonies. Uncut plasmids were screened for the presence of cDNA insert by comparing their mobility in agarose gels with the mobility of uncut wild-type pCRII vector plasmid. Selected plasmids were then restricted with the restriction enzyme EcoRI to confirm the size of the inserted cDNA fragment. EcoRI digests of F2-Sal, Sal-F2,

and F3 plasmids derived from independent transformed bacterial colonies are shown in Figure 6.

The following 15 DEN-2 16681 virus-specific cDNA clones, shown schematically in Figure 7, were selected for nucleotide sequence analysis:

	<u>Clone</u>	<u>RT/PCR</u>	
		<u>Amplicon</u>	
	1	F1	- A8
	2	F1	- A21
10	3	F1	- A25
	4	F1	- A26
	5	F2-Sal	- AA2-4
	6	F2-Sal	- AA2-8
	7	Sal-F2	- AA3-3
15	8	Sal-F2	- AA3-4
	9	F3	- AA4-4
	10	F3	- AA4-6
	11	F4	- 10
	12	F4	- 12
20	13	F5	- AA6-1
	14	F5	- AA6-2
	15	F5	- AA6-4

RT/PCR Amplification and Cloning of DEN-2 PDK-53 cDNA:

The entire genome of DEN-2 virus, vaccine strain PDK-53, was amplified from genomic RNA in the form of 23 cDNA clones of various sizes. Even though the PDK-53 vaccine contained only about 10^4 PFU/ml of virus, we were able to routinely amplify cDNA from RNA that was extracted directly from this seed virus. To accomplish this, we routinely use the "extended PCR method", incorporating the Taq extender reagent (Stratagene) in the PCR reactions. We had previously shown that the Taq extender

significantly enhanced yields of large molecular weight amplicons in the PCR amplification of the nonstructural genes of the flavivirus, St. Louis encephalitis virus (Figure 8A). For extended PCR reactions, reaction mixtures were made as for standard PCR reactions, but the standard PCR buffer was replaced with the Taq extender buffer and 1 unit of AmpliTaq DNA polymerase (Perkin-Elmer) and 1 unit of the Taq extender enzyme per kbp of expected amplicon size was included in the reaction.

Figure 8B shows the correct agarose gel migration of large cDNA amplicons F1 (containing the T7 RNA polymerase promoter at the 5' end of the mRNA-sense strand of the amplicon), F2, and F3 obtained by PCR amplification using DEN-2 PDK-53 viral genomic RNA as template. The standard PCR reaction also worked for a number of DEN-2 PDK-53 amplifications.

The PDK-53 PCR products were cloned into the pGEM-5Zf TA-vector (Promega) or the pT7Blue(R) TA-vector (Novagen). Although we seemed to have the best cloning efficiency of PCR amplicons in the pCRII TA-vector, the other vector kits were less expensive and worked well. The cloning efficiency of PCR products into the TA-vector decreased rapidly as amplicon size increased beyond 2000 bp.

The following 23 DEN-2 PDK-53 virus-specific cDNA clones were selected for nucleotide sequence analysis:

	<u>CLONE</u>	<u>RT/PCR AMPLICON</u>	<u>Expected Amplicon Length</u>	<u>Up-Amplimer</u>	<u>Down-Amplimer</u>
5	1	F-5	1552-bp	D2-SMT71	CD2-1510
	2	F1-7	"		"
	3	F1-9	"		"
	4	F1-75A	"		"
	5	F1-79B	"		"
10	6	F2-14	3355-bp	D2-1261	CD2-4615
	7	F2-16B	"		"
	8	F3-33	2676-bp	D2-4257	CD2-6932
	19	F3-3C	"		"
	10	F4-9	2373-bp	D2-6493	CD2-8865
15	11	F4.9-22	2937-bp	D2-6493	CD2-9429
	12	F4.9-53	"		"
	13	F4.5-1	1897-bp	D2-8440	CD2-10337
	14	F4.5-2	"		"
	15	F4.5-6	"		"
20	16	F4.5-7	"		"
	17	F5-72	1914-bp	D2-8773	CD2-10687.X2
	18	F5-77	"		"
	19	F5-78	"		"
	20	F3.5-4	1375-bp	D2-6046	CD2-7420
25	21	F3.5-6	"		"
	22	F3.5-19	"		"
	23	F3-3K	2676-bp	D2-4257	CD2-6932

30 Nucleotide Sequence Analyses of DEN-2 16681 cDNA Clones:

EcoRI fragments of the 15 DEN-2 16681 virus-specific cDNA clones were subcloned into the single-stranded bacteriophage M13mp18 or M13mp19 for sequencing.

35 Sequencing of the entire viral genome was performed manually using radioisotopic labeling and exposure,

development, and reading of autoradiographs. The data was read from the films and entered by hand into a sequence data spreadsheet.

The locations of observed cDNA artifacts or "errors" dictated the splicing strategy of subclones to construct the full genome-length clone. If the nucleotide at a particular position of one cDNA clone differed from the nucleotides at that same position in 2 or more independent clones, then the nucleotide in the first clone was deemed to be an error. If only 2 cDNA clones were sequenced for a given region of the genome and they differed in sequence at a particular position, then if one of the cDNA clones agreed with the sequence data of Blok et al. (1992), then the clone containing the nucleotide that was in agreement with the latter investigators was deemed to be correct. The approximate locations of the cDNA errors identified in the 16681 clones are illustrated in Figure 9.

The full genome-length cDNA clone of DEN-2 16681 virus was first constructed in pUC19. Unfortunately, RNA transcribed from this clone was not infectious. When over 90% of the full-length cDNA in the clone was resequenced, it was determined that several mutations had occurred during splicing and cloning manipulations of the subclones in *E. coli*. One of these mutations was a base deletion in the NS4B gene. This deletion would cause a frameshift of the amino acid sequence, resulting in ribosomal translation of a nonsense polypeptide downstream of the mutation point. This fatal deletion, by itself, would explain the noninfectious nature of the RNA transcribed from the first full-length clone in pUC19.

The final, correct cDNA subclones (F1-E, F2-E, F3/4/5-F) that were incorporated into the full-length, successfully-infectious clone of 16681 virus were reanalyzed by direct sequencing of the double-stranded plasmid DNA via the thermocycling method using the Taq DyeDeoxy Terminator Cycle Sequencing Kit. Sequence analysis was performed using the automated 373A DNA sequencing machine. The color-coded sequence chromatograms were read by the investigator and the data was entered manually into a computer-based spreadsheet.

We independently confirmed the sequence of the 5'-terminal 32 nucleotides of the DEN-2 16681 viral genome. A 5'-end RNA-cDNA hybrid molecule, made with primer cd2-996 and reverse transcriptase, was 3'-tailed with dCTP and annealed to dGTP-tailed, PstI-cut M13mp19 RF DNA. One of the resulting M13 clones had a cDNA run-off product containing the 5'-terminal end of the genome. The 5'-end sequence was identical to that published for DEN-2 1409 (Deubel et al., 1988) and DEN-2 16681 (Blok et al., 1992). We have not independently confirmed the sequence of the 3'-terminal 36 nucleotides of DEN-2 16681 virus or the 5'- or 3'-terminal nucleotides of DEN-2 PDK-53 virus.

We sequenced uncloned, PCR-derived amplicon cDNA fragments directly for the following regions of the DEN-2 16681 viral genome: nucleotides 70-260, 330-870, 890-1690, 1890-3720, 3770-4050, 4080-4320, and the 3'-terminal 9990-10686. Unlike the sequencing of cloned DNA, direct analysis of PCR amplicons provides sequence information for the majority population of amplified cDNA molecules,

and therefore for the majority population of template RNA molecules.

We observed very early in the project that the nucleotide sequence of DEN-2 16681 virus that we
5 determined at the CDC laboratory differed significantly from the sequence of DEN-2 16681 virus as published by Blok et al. (1992). Our nucleotide sequence differed from that published by Blok et al. (1992) at 60 nucleotide positions, which were located throughout the genome.
10 Amino acid substitutions were encoded by 26 of these nucleotide differences. The approximate genomic locations of the nucleotide differences are illustrated in the schematic diagram in Figure 10. The exact nucleotide positions of the discrepancies are shown in Figure 11.

15

Nucleotide Sequence Analyses of DEN-2 PDK-53 cDNA Clones:

The DEN-2 PDK-53 virus-specific cDNA clones were analyzed by direct sequencing of the double-stranded
20 plasmid DNA by the thermocycling method using the Taq DyeDeoxy Terminator Cycle Sequencing Kit. The 3'-end sequence from nucleotide position 10290-10686 was also determined by direct sequencing of PCR-derived amplicon cDNA. Sequence analysis was performed using the automated
25 373A DNA sequencing machine. The color-coded sequence chromatograms were read by the investigator and the data was entered manually into a computer-based spreadsheet. The approximate locations of the cDNA errors identified in the PDK-53 cDNA clones are illustrated in Figure 12.

Our determination of the nucleotide sequence of DEN-2 PDK-53 virus differed significantly from the PDK-53 genomic sequence published by Blok et al. (1992). The latter investigators reported a total of 53 nucleotide differences that encoded 27 amino acid mutations between the nucleotide sequences of the genome of DEN-2 16681 virus and that of its vaccine derivative, PDK-53 virus. They reported the following nonsilent mutations: 1 in the capsid, 2 in prM, 1 in M, 3 in E, 3 in NS1, 3 in NS2A, 2 in NS2B, 3 in NS3, 3 in NS4A, 3 in NS4B, and 3 in NS5. We detected only 8 nucleotide mutations between the genomes of these two virus strains. One mutation occurred in the 5'-NC region of the genome, while 7 nucleotide mutations, 4 of which encoded amino acid substitutions, occurred in the coding region of the genome as shown in Figure 13 and the following table.

Table: Summary of nucleotide differences between the
 genomes of DEN-2 16681 virus and its vaccine
 derivative virus, strain PDK-53.

Genome		Genome			
		Nucleotide		Amino Acid	
Position	Gene	16681	PDK-53	16681	PDK-53
57 ^a	5'-NC	C	T	-	-
524 ^a	prM-29	A	T	Asp	Val
2055 ^a	E-373	C	T	Phe	Phe
2579 ^a	NS1-53	G	A	Gly	Asp
4018	NS2A-151	C	T	Leu	Phe
5547	NS3-342	T	C	Arg	Arg
6599 ^a	NS4A-75	G	C	Gly	Ala
8571 ^a	NS5-334	C	T	Val	Val

^a 16681 vs. PDK-53 difference agrees with Blok et al.
 (1992)

The few nucleotide positions where our data and those
 of Blok et al. (1992) agreed, in terms of sequence
 differences between the 16681 and PDK-53 viral genomes,
 were distributed throughout the genome. The entire genome
 of DEN-2 16681 virus was cloned and sequenced before we
 received the PDK-53 vaccine virus at our laboratory.

Except for the 3'-terminal cDNA clones #17-#19, every PDK-53 virus-specific cDNA clone constructed in our laboratory contained at least one nucleotide position of 16681/PDK-53 sequence difference confirmed by both ourselves and Blok et al. (1992). Therefore, our PDK-53 virus-specific cDNA clones did not result from contamination of PDK-53-specific PCR reactions with 16681 virus-specific cDNA template. Our PDK-53 virus-specific cDNA clones, which also contained the many sequence discrepancies between our data and those of Blok et al. (1992), encoded the nucleotide sequence from the 5' terminus to nucleotide position 10337 of the genome of PDK-53 virus. The 3'-terminal 387 nucleotides (10337-10723) of DEN-2 PDK-53 virus were identical to those of the parental 16681 virus. Since none of the PDK-53 virus-specific cDNA clones covering this region of the genome contained a point of confirmed 16681/PDK-53 sequence difference, we repeated the PCR amplification of the 3' terminus of the PDK-53 virus genome. This was done to ensure that the 3'-terminal cDNA clones #17-#19 did not result from PCR reactions contaminated by 16681 virus-specific DNA template. The PCR reaction components were pipetted in a room in which DEN cloning had not been performed previously, using new micropipetors, newly opened pipet tips with aerosol barrier, and freshly made stock reagents. Direct sequencing of the resulting double-stranded PCR cDNA amplicon confirmed that the 3'-387 nucleotides of DEN-2 PDK-53 virus was indeed identical to the 3' terminus of the 16681 parent.

The finalized nucleotide sequence of DEN-2 virus, strain 16681, including the nucleotide and amino acid mutations identified for DEN-2 PDK-53 virus, is shown in Figure 14.

5

Construction of DEN-16681 Full-Length Clone in pUC19:

For the construction of the full genome-length cDNA clone of DEN-2 16681 virus, 5 of the sequence-
10 characterized PCR-amplified cDNA subclones were selected for splicing. However, clone #5 contained a cDNA "error" that was not readily spliced out with the existing clones. This error, which was a C-to-T mutation at nucleotide position 1730 and encoded a nonsilent Thr-to-Ile amino
15 acid substitution at E-265, was incorporated into the F2 construct. The intermediate F2 construct was the result of splicing the F2-Sal clone (#5) SphI/HpaI fragment to the Sal-F2 clone (#7) HpaI/KpnI fragment in the MCS of plasmid pUC18 (Figure 15). To correct the error, a new
20 PCR amplicon was made using primers D2-1261 and CD2-2955. Resulting clones in the TA-vector were sequenced, and the correct SphI/HpaI fragment of a new clone was substituted for the faulty SphI/HpaI fragment of the original F2 construct (Figure 16). The corrected F2 clone was
25 designated F2-C.

The relevant cDNA clones of DEN-2 16681 virus were spliced together via a series of intermediate ligation products in the MCS of pUC18 to yield F1/3/4/5, which contained all of the genome except for the SphI-KpnI 1380-
30 4493 region present in clone F2-C. Multiple attempts to

ligate the F2-C SphI/KpnI cDNA fragment into F1/3/4/5 in pUC18 failed. The cDNA insert of F1/3/4/5-pUC18 was then transferred to the MCS of pUC19, resulting in F1/3/4/5-pUC19. This operation simply reversed the orientation of the cDNA insert within the context of the pUC plasmid. Ligation of SphI/KpnI-cut F1/3/4/5-pUC19 and F2-C SphI/KpnI insert readily yielded transformants in *E. coli* X11-Blue that contained the full-length cDNA clone F1/2/3/4/5-pUC19, which was designated pD2/IC-20. The detailed splicing procedures for pD2/IC-20 are illustrated in Figure 17. The orientation-specific cloning of the full genome-length cDNA in pUC19 rather than pUC18 is diagrammed in Figure 18.

The full genome-length cDNA of DEN-2 16681 virus was cloned into the MCS of pUC19. Apparent full genome-length viral mRNA was transcribed from linearized pD2/IC-20. This transcribed product failed to yield infectious virus following electroporation of BHK-21 cells. Most of the cDNA in the pD2/IC-20 clone was resequenced, and several cloning artifacts, including a fatal single-nucleotide deletion, were identified. Original subunit intermediate cDNA constructs in pUC18 were resequenced to confirm that they possessed the correct sequence and corrected where necessary. The corrected primary cDNA clones F1, F2-C, and F3/4/5 were then ligated into the low-copy plasmid pBR322, rather than the high copy-number pUC18 plasmid. It was envisioned that the cDNA would be more stable in a slower-replicating plasmid in *E. coli*.

To enable more straightforward cloning into pBR322, the MCS of pUC19 was spliced into the pBR322 plasmid

(Figure 19). This resulted in plasmids pBRUC-138 and pBRUC-139 containing the pUC MCS in both orientations within the pBR322 plasmid backbone. The SphI site was removed from both pBRUC plasmids by cutting with SphI, blunt ending of the cut ends using T4 DNA polymerase, and then ligating the ends back together. This was necessary for the construction of the full-length cDNA clone because SphI is one of the cDNA restriction/splicing sites for the clone.

The F3/4/5-F cDNA clone of DEN-2 16681 virus, which had been verified by sequence analysis, was cloned into pBRUC-139 (SphI-) (Figure 20). Following this ligation, the F1-E and F2-C cDNA clone fragments were also moved into the pBR322 backbone to construct the full genome-length cDNA clone, pD2/IC-30P (Figure 20). This recombinant plasmid was replicated successfully in both TB-1 and MC-1061 strains of *E. coli*.

Construction of DEN-2 PDK-53 Infectious cDNA Clone:

The full-length infectious clone of DEN-2 16681 virus was used in the construction of the infectious clone for PDK-53 virus. Since the 3'-noncoding regions of the genomes of both viruses are identical, and the amino acid sequences of the translated precursor polyproteins encoded by genome nucleotide positions 6646-10269 are identical in both viruses, the infectious clone of PDK-53 virus was constructed using the 16681 3'-end cDNA from the NheI site at nucleotide position 6646 to the 3' terminus of the genome (Figure 21). After correcting a cDNA error in the

PDK-53 F3-3C subunit clone, this fragment and the F2-16B cDNA fragment were ligated into the infectious clone backbone to construct the DEN-2 PDK-53 virus-specific full-length cDNA clone, pD2/IC-130V (Figure 21).

5

Transcription of Viral mRNA from DEN-2 Infectious cDNA Clones:

Viral genomic RNA extracted from gradient-purified virions was analyzed by nondenaturing RNA agarose gel electrophoresis to observe the level of RNA degradation and the limits of detectability by ethidium bromide staining. Figure 22 shows an agarose gel electropherogram for 22-383 ng of viral genomic RNA obtained from purified preparations of wild-type DEN-2 16681 virus and wild-type Venezuelan equine encephalitis (VEE) virus, strain Trinidad donkey. Although degradation of the RNA is visible as a spectrum of smaller molecular weight nucleic acid (smear in Figure 22), definite full-genome length RNA bands are clearly visible. This smear of nucleic acid is probably also due, in part, to multiple conformations of the single-stranded RNA molecules which migrate through the gel at different rates. The relative gel migration of the single-stranded RNA does not correlate directly with the sizes of the double-stranded molecular weight marker DNA bands (MW, Figure 22); the VEE and DEN-2 viral genomes are 11,447 and 10,723 nucleotides in length, respectively. BHK-21 and C6/36 cells were transfected successfully by electroporation with 2000, 500, 100, 10, 1, and 0.1 ng of viral genomic RNA extracted from purified VEE or DEN-2

16681 virus, as indicated by development of CPE, expression of viral proteins detected by indirect immunofluorescence tests using virus-specific antibody, and/or by plaque titration of infectious virus from the transfected-cell culture medium. RNA quantities of 1 ng or less were essentially undetectable in the ethidium bromide-stained agarose gel system we used. Therefore, authentic RNA transcripts derived from full genome-length cDNA and visualized in agarose gel electropherograms of transcription reactions should be infectious for BHK-21 cells by electroporation.

Investigators previously constructed an infectious cDNA clone for VEE virus as reported by Kinney et al. (1989). RNA transcription reaction conditions that yielded high quantity and quality of infectious mRNA transcripts from the pVE/IC-92 infectious clone of VEE virus failed in multiple attempts to transcribe RNA from the pD2/IC-20 clone of DEN-2 16681 virus. Figure 23 shows an agarose gel electropherogram that demonstrates successful transcription of RNA from the VEE clone, but not pD2/IC-20.

In an attempt to improve RNA transcription from the DEN-2 clone, commercial transcription kits were purchased. The Megascript transcription kit supplied by Ambion also failed to transcribe RNA from the DEN clone. However, the Ampliscribe kit obtained from Epicentre Technologies enabled efficient transcription of RNA from the DEN-2 clone (Figure 24).

The success of the Ampliscribe kit apparently was due to the high concentration of ribonucleotides and a very

high, but proprietary, concentration of T7 RNA polymerase. The RNA transcribed from pD2/IC-20 was not infectious. However, viral mRNA transcribed from DEN-2 16681 clone pD2/2-IC30P and PDK-53 clone pD2/IC-130V was infectious
5 (Figure 25).

Viral mRNA transcripts from both replicates of pD2/IC-30P (A and D) and pD2/IC-130V (F and J) were infectious, producing viable infectious virus in electroporated BHK-21 cells. Figure 26 shows RNA
10 transcripts from pD2/IC-20, pD2/IC-30P, and pD2/IC-130V.

Construction of DEN-2 16681/PDK-53 Chimeric cDNA Clones:

Several chimeric full-length cDNA clones were derived
15 from the pD2/IC-30P and pD2/IC-130V clones. All clones were constructed in the pBRUC-139 derivative of the pBR322 plasmid vector. *E. coli* strains XL1-Blue, MC-1061, and TB-1 were successfully transformed with ligated recombinant plasmids containing full genome-length cDNA.
20 Viable virus was derived from all of the indicated clones. The evolutionary tree for the chimeric viruses is diagrammed in Figure 27.

Details concerning the splicing strategies for the chimeric clones are shown in Figure 28. Appropriate cDNA
25 fragments were cut and ligated together at the internal SalI, SphI, KpnI, and NheI sites as well as at the 5'-SstI and 3'-XbaI sites.

Viable prototype and chimeric viruses were derived from each of the clones indicated in Figure 28 by
30 electroporation of BHK-21 cells with viral genome-length

mRNA transcribed from linearized plasmids. Seed stocks of these viruses were prepared by centrifuge-clarification of the cell culture medium, adjustment of the FBS concentration to 10%, and freezing of seed aliquots at 5 -70°C. Virus concentrations were determined by plaque titration of the virus seeds in monolayer cultures of Vero cells. The results of these virus titrations are shown in the following table.

Table. Plaque titration of DEN-2 16681 and PDK-53 stock seed viruses and chimeric viruses recovered from BHK-21 cells transfected with infectious clone-derived viral mRNA transcripts.

Virus	(PFU/ml)	Genotype ^a
DEN-2 16681	8.0 X 10 ⁷	c D F G L R G V
DEN-2 PDK-53	5.1 x 10 ³	t V . D F . A .
D2/IC-30P-A	3.6 X 10 ⁵
D2/IC-30P-A2	1.7 X 10 ⁵
D2/IC-130V-F	4.0 X 10 ⁵	t V . D F . A .
D2/IC-130V-J	2.2 X 10 ⁵	t V . D F . A .
D2/IC-130V2-1	2.8 X 10 ⁵	t V A .
D2/IC-130V2-7	8.8 X 10 ⁴	t V A .
D2/IC-31-12	2.1 X 10 ⁵	t V
D2/IC-31-15	3.2 X 10 ⁵	t V
D2/IC-32-A	1.4 X 10 ⁶	. . . D F . . .
D2/IC-32-G	1.2 X 10 ⁶	. . . D F . . .
D2/IC-33-C	9.6 X 10 ⁴ A .
D2/IC-33-P	1.9 X 10 ⁵ A .
D2/IC-321-L	1.1 X 10 ⁶	t V . D F . . .
D2/IC-321-N	7.6 X 10 ⁵	t V . D F . . .
D2/IC-323-B	7.2 X 10 ⁵	. . . D F . A .
D2/IC-323-I	8.8 X 10 ⁵	. . . D F . A .
D2/IC-31-57-5	2.4 X 10 ⁵	t
D2/IC31-524-D	3.2 X 10 ⁴	c V

^a Genotype is designated in small case for the virus-specific 5'-noncoding nucleotide and in upper case single-letter amino acid abbreviation for amino acids encoded by virus -specific nucleotide mutations. Dots represent nucleotide or amino acid sequence identity with DEN-2 16681 virus.

To establish the validity of the clone-derived chimeric viruses, relevant genomic cDNA fragments were amplified directly from seed viruses by PCR and spot-sequenced. The results are shown in Figure 29. This validation process is ongoing. Except for D2/IC-31-524 virus, appropriate cDNA insert regions in chimeric viruses have been confirmed by sequence analysis. Except for D2/IC-30P, D2/IC-130V, and D2/IC-31-57, which have been fully confirmed, clone-derived chimeric viruses have yet to be spot-sequenced in a recipient clone-derived cDNA region to definitely establish the chimeric nature of the virus. The recipient clone is the recombinant plasmid backbone into which a cDNA fragment, the insert fragment, from a heterologous donor clone is spliced. Where duplicate clone-derived viruses were obtained, both viruses of a given genotype were spot-sequenced, and both gave the same result, which is shown in Figure 29.

Submission of pD2/IC-30P and pD2/IC-130V to ATCC:

20

Patent deposits of the full genome-length cDNA clones of DEN-2 16681 and PDK-53 viruses were submitted to the American Type Culture Collection (ATCC), Rockville, Maryland, U.S.A. Both pD2/IC-30P-A and pD2/IC-130V-F were grown overnight in *E. coli* TB-1 cells. Six cryogenic vials containing 1 ml each of frozen cell culture in 10% glycerol were submitted by dry ice shipment. Prior to shipment, plasmid was extracted from a 1 ml aliquot of each virus-specific culture. The recombinant full-length

plasmid was recovered from the cells as shown in Figure 30.

The pD2/IC-30P-A deposit with the ATCC was assigned accession number ATCC 69826, and the pD2/IC-130V-F deposit with the ATCC was assigned accession number ATCC 69825. Date of deposit was May 25, 1995.

Construction of Chimeric DEN-2/1, -2/3, and -2/4

Infectious Clones:

10 We contemplate deriving chimeric DEN-2/1, DEN-2/3, and DEN-2/4 viruses from recombinant full genome-length cDNA clones containing the genetic background of DEN-2 PDK-53 virus and the prM and E genes of the DEN-1, DEN-3, and DEN-4 candidate vaccine viruses, respectively. To
15 accomplish this, the prM and E genes of the vaccine viruses were amplified by PCR. Because our laboratory has been establishing a sequence database to analyze the molecular epidemiology of several flaviviruses, including all of the serotypes of dengue virus, the primers used for
20 cDNA amplification in the PCR were readily available at our laboratory. The amplified cDNA molecules were sequenced directly, thus providing the sequence of the population of virions in the virus seed. The amplified cDNA amplicons for the DEN-1, DEN-3, and DEN-4 vaccine
25 viruses have all been cloned into the pGEM-5Zf TA-vector. The cloned cDNA has not been analyzed by sequencing, since it will be necessary to rederive the cDNA amplicons by PCR to incorporate appropriate RENZ cleavage sites within the amplicon for splicing into the full-length cDNA backbone
30 of DEN-2 PDK-53 virus. The partial nucleotide sequences

of the genomes of the DEN-1, DEN-3, and DEN-4 vaccine viruses were aligned with the DEN-2 PDK-53 sequence. All four sequences are aligned with the nucleotide sequence of DEN-2 16681 virus and its deduced amino acid sequence in Figure 31. The deduced amino acid sequences of the DEN viruses are aligned in Figure 32.

It is readily evident from the aligned nucleotide sequence data that useful restriction enzyme sites in the DEN-2 virus-specific cDNA are not conserved in the DEN-1, DEN-3, and DEN-4 viruses. Therefore, splicing sites must be engineered into the cDNA to enable the splicing of heterotypic DEN-1, DEN-3, and DEN-4 prM and E genes into the DEN-2 backbone. It is not yet clear precisely how the nonstructural proteins of flaviviruses interact with the structural proteins during intracellular maturation of the virus. Furthermore, the interaction of the capsid protein with the genomic mRNA molecule in the nucleocapsid of the virion has not been defined. However, coexpression of the E and prM proteins has been more successful than expression of E alone in expression systems *in vitro*. The DEN-2 nonstructural proteins are involved in all virus-specific intracellular polyprotein processing and replication of viral mRNA, and the predominant portion of the mRNA genome interacting with the capsid protein is presumably, but not necessarily, DEN-2 virus-specific. For these reasons, our strategy is to splice in the prM and E genes of DEN-1, DEN-3, and DEN-4 viruses very precisely, while maintaining the DEN-2 context of the bracketing capsid and NS1 protein regions.

The strategies for creating XhoI and XbaI splice sites at the 5' end of the prM gene and near the 3' end of the E gene are illustrated in detail in Figures 33 and 34, respectively. Briefly, mutagenic primers containing the appropriate RENZ site are utilized in PCR reactions to synthesize new cDNA for the prM and E genes of all four viruses. A DEN-2 PDK-53 virus-specific cDNA cassette plasmid, designated pD2V-CAS12, containing the genome region from the 5' terminus through nucleotide position 4696 is constructed via intermediate plasmid constructs pF1-Xho and pF2-Xba as illustrated in Figures 35 and 36. The XhoI/XbaI cDNA fragments cut directly from DEN-1, DEN-3, and DEN-4 virus-specific amplicons synthesized by PCR using the mutagenic primers are ligated into the pD2V-CAS12 cassette plasmid to create subclone chimeras. The SstI/KpnI fragment of the resulting pD1V-CAS12, pD3V-CAS12, and pD4V-CAS12 cassettes are moved into pD2/IC-130V restricted with SstI/KpnI to create the chimeric full genome-length cDNA clones (Figure 36).

Discussion:

Infectious cDNA clones permit the directed engineering of viral genomes. Depending on their viability in terms of ability to replicate in cell culture, infectious clone-derived viruses can be modified by incorporating point mutations, multiple mutations, deletions, gene regions of related or heterologous viruses, or nonviral genes. Infectious cDNA clones have been developed for many RNA viruses, including flaviviruses DEN-4 (Lai et al., 1991), yellow fever (Rice

et al., 1989), Kunjin (Khromykh and Westaway, 1994), Japanese encephalitis (Sumiyoshi et al., 1992), and TBE (unpublished data). We describe herein the development of infectious cDNA clones for DEN-2 16681 virus and its candidate vaccine derivative, strain PDK-53. We also describe the construction of chimeric viruses, incorporating the prM and E genes of candidate DEN-1, DEN-3, and DEN-4 vaccine viruses within the genetic background of the DEN-2 PDK-53 vaccine virus.

Although the candidate vaccine viruses developed at Mahidol University are currently the best live DEN virus vaccine candidates in terms of immunogenicity and safety in adult humans, the DEN-1, DEN-3, and DEN-4 vaccine viruses replicate poorly in cell culture and possess low infectivity in humans, requiring up to 2000-fold more PFU of virus to infect and immunize humans than is needed for the DEN-2 PDK-53 vaccine virus. The low infectivities of these viruses have significant implications for vaccine production in cell culture, potentially decreased immunogenic efficacy, and more rapid inactivation under conditions of a poorly maintained cold chain in tropical countries where dengue viruses are endemic.

The purpose of engineering chimeric DEN vaccine viruses is to enhance the replicative ability and immunogenicity of the DEN-1, DEN-3, and DEN-4 vaccine viruses. A primary assumption has been that the attenuated DEN-2 PDK-53 vaccine virus replicates to appropriate levels in cell culture. In fact, it does appear that the genome of DEN-2 PDK-53 virus is eminently suited to serve as the genetic backbone for chimeric

viruses containing the prM and E genes of DEN-1, DEN-3, and DEN-4 vaccine viruses. We have recently completed growth curves for DEN-2 16681 virus, DEN-2 PDK-53 virus, and their infectious clone derivative viruses in LLC-MK₂ cells.

The viruses were titrated in Vero cell monolayers. These data are shown in the following table:

Virus	Maximum Titer (PFU/ml)	Maximum Titer at Day
DEN-2 16681	2.6×10^8	10
D2/IC-30P-A	1.7×10^7	8
D2/IC-30P-A2	6.6×10^7	7
DEN-2 PDK-53	3.8×10^7	9
D2/IC-130V-F	2.9×10^7	7
D2/IC-130V-J	1.7×10^7	7

The DEN-2 PDK-53 virus and its infectious clone derivative viruses grow to approximately 10^7 PFU/ml in LLC-MK₂ cells, about as well as the DEN-2 16681 virus.

A second assumption is that the chimeric DEN viruses will be viable and the DEN-2 PDK-53 virus-specific replication machinery will significantly increase replication of the chimeric viruses in cell culture and increase their infectivity and immunogenicity in humans relative to the wild-type vaccine viruses. The high degree of conservation of amino acid sequences among the polyproteins of the four DEN viruses should ensure that the chimeric viruses will be viable. The level of

replication attained by the chimeric DEN viruses is determined empirically, as was determined for the DEN-2 PDK-53 infectious clone derivative virus.

Bray et al. (1991) constructed chimeric DEN-4/1 and
5 DEN-4/2 viruses that appeared to appropriately express
DEN-1 and DEN-2 structural protein antigens in the genetic
background of DEN-4 virus. These investigators spliced
much of the 5'-noncoding region, and the capsid, prM and E
genes of DEN-1 or DEN-2 virus into the full-length cDNA
10 clone of DEN-4 virus. The near 3'-terminal splice site
they chose in the E gene is very close to that proposed by
us in our project. These chimeric viruses replicated very
slowly relative to the wild-type viruses. The authors
attributed this slow replication to possible suboptimal
15 gene expression, assembly, and/or maturation due to
incompatibility of heterotypic genes or RNA packaging in
the nucleocapsid. Another possibility is that cDNA errors
may have been incorporated into their constructs. In
contrast, Pletnev et al. (1993) engineered chimeric
20 viruses between DEN-4 virus and tick-borne encephalitis
(TBE) virus, which is a very distant flavivirus relative
of DEN viruses. Thus, DEN virus chimeras may be derived
that are viable.

A third assumption is that our chimeric DEN viruses
25 will express the appropriate structural protein antigens
of DEN-1, DEN-3, and DEN-4 viruses, and that vaccinees
will respond with development of appropriate serum titers
of DEN-1, DEN-3, and DEN-4 neutralizing antibodies
following immunization with the chimeric viruses. We
30 describe the insertion of the prM and E genes of DEN-1,

DEN-3, and DEN-4 viruses into the DEN-2 clone. Thr-to-Ser amino acid substitutions near the amino terminus of the prM protein in DEN-2, DEN-2/1, DEN-2/3, and DEN-2/4 viruses resulting from mutagenesis to create the XhoI site of the cassettes should be conservative in nature and affect the phenotype of derived viruses minimally, if at all. Alternatively, a unique MluI site (ACGCGT) could be created via a single, silent A-to-G point mutation at nucleotide position 453 in the DEN-2 clone. The MluI site immediately preceding the T7 promoter could easily be eliminated by cutting the clone with MluI, blunt-ending, and religation. The clone-derived DEN-2 and chimeric viruses would then have the prM amino-terminal sequence "FHLTTR."

15 The carboxyl-terminal 24 amino acids of the E glycoprotein of all of the infectious clone-derived viruses will be those of the DEN-2 PDK-53 virus. Therefore, the E protein of all of the chimeric viruses will have amino acid mutations in this region. Yet, the carboxyl-terminal 39 amino acids of the DEN virus E protein comprise membrane-spanning, transmembrane domains. In all enveloped viruses, the transmembrane domains of the integral viral proteins of related viruses are quite variable in amino acid sequence. It has often been noted that the important conserved feature of amino acids in this domain lies in their hydrophobic, "lipid-loving" nature rather than in the absolute sequence. Creation of a MroI site (TCCGGA) or a unique AgeI site (ACCGGT) at nucleotide positions 2281-2286 in the DEN-2 clone would

result in amino acids "SG" or "TG", respectively, at positions E-449 and E-450 in the clone-derived viruses.

The E protein of all flaviviruses share a similar gross tertiary structure that is indicated by the absolute conservation of the 6 Cys residues in the prM protein and
5 in the 12 Cys residues in the ectodomain (the region located on environment side of the viral lipid envelope) of the E protein of DEN, Japanese encephalitis, West Nile, Murray Valley encephalitis, St. Louis encephalitis,
10 Kunjin, yellow fever, TBE, Langat, and Powasson flaviviruses (data not shown). Cys residues are involved in intrachain Cys-Cys disulfide bonds that determine the overall structure of the protein. We fully expect the DEN-2/1, DEN-2/3, and DEN-2/4 chimeric viruses to be
15 viable and to replicate more efficiently than the wild-type DEN-1, DEN-3, and DEN-4 vaccine viruses, respectively. Furthermore, chimeric recombinants involving the genetic backbone of one flavivirus and the structural genes of a variety of different flaviviruses
20 may also be viable, as has been demonstrated for DEN-4/TBE virus recombinants (Pictnev et al., 1993). Such recombinant viruses offer the potential opportunity to engineer chimeric vaccine viruses for a number of flavivirus-associated diseases within the genetic
25 background of a single flavivirus. The X-ray crystallographic structure of the E glycoprotein of TBE flavivirus has recently been published (Rey et al., 1995). This development has significant implications for the future design of flavivirus molecular vaccines.

A fourth assumption is that the chimeric DEN viruses will retain the attenuated phenotype of the wild-type DEN-1, DEN-3, and DEN-4 vaccine viruses, despite enhanced replicative efficacy provided by the more efficient nonstructural genes and 5' and 3' noncoding regions of the DEN-2 PDK-53 virus. This presupposes that DEN-2 PDK-53 virus has attenuating mutations in the noncoding regions or in the nonstructural genes and/or that attenuating mutations occur in the prM/E region of the genomes of DEN-1, DEN-3, and DEN-4 viruses. Mutations in essentially any region of the viral genome may be capable of attenuating a virulent virus. This has been demonstrated for a number of viruses including polio virus, VEE virus, and Theiler's virus. Noncoding as well as protein coding regions may be involved in attenuation. Attenuating mutations in the envelope proteins of enveloped viruses are common (Barrett et al., 1990).

The nucleotide mutations in DEN-2 PDK-53 virus at genome nucleotide positions 57 (5'-noncoding region), 524 (prM), 2579 (NS1), 4018 (NS2A), and 6599 (NS4A) may be involved in attenuation of the virus. Unless the prM amino acid mutation is the only mutation affecting virulence of the virus, the DEN-2 PDK-53 genetic background, within which the structural genes from heterologous viruses will be expressed, does itself possess genotypic markers of attenuation. We can determine the genetic loci involved in the attenuation of the DEN-2 PDK-53 virus by analyzing DEN-2 16681/PDK-53 recombinant viruses derived from chimeric 16681/PDK-53

full-length clones. The E gene of DEN-2 PDK-53 virus contains no attenuating mutations.

Although investigators have sequenced the structural genes of numerous DEN-3 virus strains (e.g., Lanciotti et al., 1994), none have sequenced the DEN-3 16562 virus, parent to the DEN-3 PCMK-30/FRhL-3 vaccine virus. After determining the sequences of the prM and E genes of this virus, we can establish if any amino acid mutations have occurred within these genes in the DEN-3 vaccine virus.

By comparison, nucleotide sequence information for the parental DEN-1 and DEN-4 viruses have been determined (unpublished data (parental DEN-1 virus); Lanciotti et al., submitted for publication (parental DEN-4 virus)). The nucleotide sequences of the E gene of DEN-4 1036 virus and both prM and E genes of DEN-1 16007 virus have been determined. The following amino acid mutations were identified:

Virus type	E Protein Amino Acid Position	Amino Acid	
		Parent Strain	Vaccine Strain
DEN-1	E-130	Val	Ala
	E-203	Glu	Lys
	E-204	Arg	Lys
	E-225	Ser	Leu
	E-384	Ala	Glu
	E-477	Met	Val
DEN-4	E-345	Glu	Lys
	E-364	Val	Ala

There were six amino acid mutations in the E protein of DEN-1 16007 PDK-13 virus and 2 mutations in that of DEN-4 1036 PDK-48 virus. There were no amino acid substitutions in the prM protein of the DEN-1 vaccine virus. Glu-to-Lys and Lys-to-Glu amino acid substitutions, as occur at DEN-1 E-203 and DEN-4 E-345, are common motifs in sequence comparisons between parent viruses and their vaccine derivatives. It is likely that the heterologous prM/E cDNA inserts in recombinant full-length cDNA clones will transport genetic loci of attenuation into the chimeric DEN-2/1, DEN-2/3, and DEN-2/4 virus derivatives. The optimum scenario for the chimeric viruses involves increased replication ability in the presence of genetic loci of attenuation in the heterologous DEN-1, DEN-3, and

DEN-4 structural gene inserts within the genetic background of the DEN-2 PDK-53 virus.

Nucleotide sequence analysis of expressed genes is essential. The error rate in the original RT/PCR derived
5 cDNA clones of DEN-2 16681 virus was 8.2×10^{-4} , that is 1 cDNA error for every 1227 nucleotides of cloned, sequenced cDNA. In a previous sequencing project involving VEE virus and employing classical, non-PCR cDNA synthesis methodology, the error rate was calculated to be 3.9×10^{-4}
10 or 1 error for every 2543 nucleotides of cloned, sequenced cDNA. These errors are due to nucleotide incorporation errors by reverse transcriptase during first strand cDNA synthesis and perhaps to the cloning of individual variants within the original population of virions.
15 Unlike many DNA polymerases, RNA polymerases and reverse transcriptase have no editing function. Incorrect nucleotides incorporated during strand elongation are not detected or removed before continuing. The Taq DNA polymerase is also known to incorporate errors into PCR
20 amplicons. Thus, at least 4-8 cDNA "errors" can be expected to occur in 10 kb of cloned cDNA. We have observed the incorporation of spurious in-frame termination codons (TAA, TAG, TGA) in cDNA clones derived from both VEE and DEN viruses. Premature termination of
25 amino acid translation would result in a truncated protein and would undoubtedly be a lethal mutation for a candidate infectious clone. Much of the utility of genes expressed in vitro is compromised when those genes are not characterized by sequence analysis. If cDNA errors occur
30 in candidate infectious cDNA clones, it may be difficult

to determine if phenotypic effects of directed mutations are due to the engineered mutation, to cDNA errors, or to synergistic action or compensation between errors and engineered mutations.

5 Wiktor et al. (1984) reported that two cDNA errors caused spurious amino acid substitutions in rabies virus glycoprotein expressed in recombinant vaccinia virus and resulted in expression of non-authentic rabies glycoprotein. After sequence analysis and correction of
10 the cDNA, expression of authentic rabies glycoprotein was obtained. A faulty cDNA clone may behave as expected in one circumstantial context, yet behave very inappropriately and be highly misleading in a different context. A faulty structural gene cDNA clone of the
15 virulent VEE Trinidad donkey (TRD) virus that was expressed in recombinant vaccinia virus was essentially authentic by monoclonal antibody analysis of expressed VEE virus-specific proteins and by protection of immunized mice from challenge with virulent VEE virus (Kinney et
20 al., 1988a; Kinney et al., 1988b). However, incorporation of this cDNA clone into an infectious cDNA clone of VEE virus completely abrogated the virulence of the clone-derived virus, whereas the corrected cDNA fragment resulted in derivation of virulent virus (Kinney et al.,
25 1993).

Although Lai et al. (1991) originally derived their infectious clone of DEN-4 virus from sequence characterized subunit cDNA clones (Zhao et al., 1986; Mackow et al., 1987), the original full-length clone was
30 not infectious (Lai et al., 1991). While these

investigators indicated that they sequenced both strands of much of the cloned genomic cDNA, they did not indicate that they sequenced more than a single clone for a given cDNA region. Nucleotides encoding cDNA errors will be confirmed on both cDNA strands, but will not be identified as errors unless the sequences of two or more independent cDNA clones covering the same region of the genome are sequenced. The functional full-length clone of DEN-4 virus was obtained by repeated splicing of large new cDNA fragments into the full-length clone until a functional clone was obtained. The authors did not indicate that the newly cloned regions were characterized by nucleotide sequence analysis (Lai et al., 1991). It is probable that the slowed replication of the DEN-4/1 and DEN-4/2 chimeric viruses relative to wild-type viruses reported by Bray et al. (1991) is due to the presence of cDNA artifacts within the full-length cDNA clone. The critical importance of accurate nucleotide sequence characterization of genes expressed *in vitro*, particularly when those genes are expressed in the form of infectious cDNA clones, is still not widely appreciated by many in the molecular biology field.

Although putative nucleotide sequences for the genomes of DEN-2 16681 and DEN-2 PDK-53 viruses have been reported in the literature (Blok et al., 1992), our sequence results indicate that the published data is highly flawed. Blok et al. (1992) reported 53 nucleotide mutations between the two viruses; we determined only 8 mutations. We analyzed at least two independent cDNA clones for regions covering the entire genomes of both

viruses. The DEN-16681 sequencing project was completed prior to receiving the DEN-2 PDK-53 virus in our laboratory, and the nucleotide sequence of the PDK-53 virus was determined from cDNA amplified directly from virus present in vaccine vials.

There are now only two classes of infectious clones developed for vaccine flaviviruses that have themselves been administered to humans: the infectious clone of yellow fever virus, vaccine strain 17D (Rice et al., 1989; Hahn et al., 1987; Rice et al., 1985), and the DEN-1, DEN-2, DEN-3, and DEN-4 vaccine derivative infectious clones described herein. Both classes of infectious clones have the important advantage of being derived from vaccine viruses that have been tested for efficacy and safety in humans. The yellow fever 17D virus vaccine has long been one of the most effective human vaccines developed; immunization with this virus provides lifelong immunity. In the case of DEN virus, it is essential that vaccines provide immunity against infection by all four serotypes of the virus. DEN-1, DEN-2, DEN-3, and DEN-4 vaccine viruses have been developed at Mahidol University, Bangkok, Thailand. All four vaccine viruses have been tested in humans and have been demonstrated to be immunogenic and safe for human adults.

Replicating vaccines in the form of live, attenuated viruses offer distinct advantages in terms of immunogenic efficacy due to replicative amplification of viral antigens (antigenic mass) in the vaccinees and replication in appropriate target tissues. Inactivated or subunit antigens usually suffer from a lack of sufficient

antigenic mass and subsequent failure to stimulate an effective immune response. Expression of proteins in recombinant vaccinia virus, which replicates primarily at the site of inoculation, may provide protection against parenteral challenge with virulent virus, but may not protect against an aerosol challenge. This was demonstrated for VEE virus when it was shown that recombinant vaccinia virus expressing the structural proteins of VEE virus protected mice from intraperitoneal challenge, but not intranasal challenge, with virulent VEE virus (Kinney et al., 1988b). Immunization with the live, attenuated VEE TC-83 vaccine virus, on the other hand, provided immunity against both parenteral challenge (immunity provided by circulating serum IgG antibody) and intranasal challenge (mucosal, IgA-base immunity) with virulent VEE virus. Furthermore, the level of immunity, as measured by titers of VEE virus-specific neutralizing antibody, were considerably higher in TC-83 virus-immunized mice and horses (the natural epidemic host for VEE virus) than in animals immunized with recombinant vaccinia/VEE virus (Kinney et al., 1988b; Bowen et al., 1992). Similar results have been reported for vaccinia/influenza A virus recombinants in rodents (Smith et al., 1986). Furthermore, a replicating vaccine virus provides the appropriate T-cell epitopes to stimulate cell-mediated immunity as well as humoral immunity. T-cell epitopes may be lacking in subunit vaccines. In short, vaccination with a safe live, attenuated vaccine virus provides the optimal immunization of a natural infection in terms of the type and level of immunity

elicited and the repertoire of viral antigens involved in generating the immune response.

To use the DEN viruses described herein as vaccine candidates, it is necessary to rederive the viruses by transfection of a cell line, such as primary dog kidney, certified for human use under conditions of good laboratory practice and management to ensure the avoidance of potential adventitious agents that might be present in uncertified cell lines. Although the cDNA-derived viruses originate from candidate vaccine viruses that have undergone testing in humans, they require recertification by analysis for possible *in vitro* phenotypic markers of attenuation and by safety testing in small animals and probably nonhuman primates. All investigative studies involving the pathogenesis of DEN virus are hampered by the unavailability of a suitable animal model. Certain *in vitro* characteristics are apparently associated with attenuation of DEN viruses, but the only definitive test is vaccine trial in human volunteers. Vaccine trials would presumably follow those of the original wild-type vaccine viruses developed at Mahidol University. The protocol includes titration of the individual vaccine virus candidates in adult human volunteers to determine the minimal infectious/immunogenic dose for each virus. This is followed by immunization trials with different bivalent and trivalent combinations of vaccine virus. The final test is the quadravalent vaccine composed of appropriate doses of all four vaccine viruses. If the preliminary trials are successful, larger trials are scheduled, and the vaccine viruses are tested in children,

who are the primary target for vaccine delivery.

We describe herein a preferred method to develop an infectious cDNA clone for a flavivirus. Optimally, a wild-type vaccine virus serves as the template for the clone construction. Large cDNA fragments are amplified from the genomic mRNA by PCR using virus-specific primers and directly cloned into a TA-vector or into the MCS of a low-copy number plasmid following restriction of the amplicon cDNA. The low-copy pBRUC-139 vector contains the MCS of pUC19 to permit convenient cloning of cDNA using a variety of RENZ sites. Other low-copy plasmids are available. The bacteriophage T7 or SP6 promoter is usually engineered into the 5'-terminal mRNA-sense amplicon, and a unique RENZ site for linearization of the recombinant plasmid containing the full-length cDNA must be engineered into the 3-terminal complementary (negative)-sense amplicon. Exhaustive nucleotide analysis of the cDNA clones is desirable.

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15

APPENDIX APRIMERS DESIGNED FOR DEN-2 CLONING/SEQUENCING PROJECT:

SEQ. ID	PRIMER	MER/SENSE	SEQUENCE
NO:			
3	pUC/M13-P5	25/+	5'-CCCAGTCACGACGTTGTAAAACGAC-3'
4	pUC/M13-P5B	27/+	5'-GGATGTGCTGCAAGGCGATTAAAGTTGG-3'
5	pUC/M13-P3	25/+	5'-TGAGCGGATAACAATTTACACAGG-3'
6	pUC/M13-P3B	27/-	5'-GGCTTTACACTTTATGCTTCCGGCTCG-3'
7	D2-1-ECO.T7 75/+		5'-GCGGATATTG/GAATTC/TCTAGA/ AATTTAATACGACTCACTATA/ AGTTGTTAGTCTACGTGGACCGACAAAGACAG-3' (5'-Fill /EcoRI /XbaI/T7 Promoter/ 5'-end of DEN-2)
8	D2-SMT71	77/+	5'-CCAGT/GAATTC/GAGCTC/ACGCGT/ AAATTTAATACGACTCACTATA/ AGTTGTTAGTCTACGTGGACCGACAAAGACAG-3' (5'-Fill/EcoRI/SstI/MluI/T7 Promoter/ 5'-end of DEN-2)
9	D2-1	24/+	5'-AGTTGTTAGTCTACGTGGACCGAC-3'
10	D2-28	34/+	5'-GACAGATTCTTTGAGGGAGCTGAGCTCAACGTAG-3'
11	D2-134	28/+	5'-TCAATATGCTGAAACGCGAGAGAAACCG-3'
12	cD2-250	26/-	5'-GGGATTGTTAGGAAACGAAGGAACGC-3'
13	D2-274	32/+	5'-CCACCAACAGCAGGGATACTGAAAAGATGGGG-3'
14	cD2-378	25/-	5'-TGCAGATCTGCGTCTCCTATTCAAG-3'
15	D2-528	25/+	5'-CGTGAACATGTGTACCCTCATGGCC-3'
16	cD2-616	26/-	5'-TTGCACCAACAGTCAATGTCTTCAGG-3'
17	D2-616	25/+	5'-ACCAGAAGACATAGATTGTTGGTGC-3'
18	cD2-618	25/-	5'-GCACCAACAGTCTATGTCTTCTGGC-3'
19	cD2-771	25/-	5'-ATGTTTCCAGGCCCTTCTGATGAC-3'
20	D2-847	25/+	5'-GCAGCAATCCTGGCATAACCATAG-3'
21	D2-996	27/+	5'-GGTTGACATAGTCTTAGAACATGGAAG-3'
22	cD2-996	27/-	5'-CTTCCATGTTCTAAGACTATGTCAACC-3'

SEQ. ID		101	
NO:	PRIMER	MER/SENSE	SEQUENCE
23	D2-1005	35/+	5'-GTCTTAGAACATGGAAGTTGTGTGACCACGATGGC-3'
24	D2-1141	25/+	5'-ACAACAGAATCTCGCTGCCCAACAC-3'
25	D2-1211	25/+	5'-GCAAACACTCCATGGTAGACAGAGG-3'
26	cD2-1211	25/-	5'-CCTCTGTCTACCATGGAGTGTTTGC-3'
27	cD2-1227	27/-	5'-CCACATCCATTTCCCCATCCTCTGTCT-3'
28	D2-1261	30/+	5'-GGAAAGGGAGGCATTGTGACCTGTGCTATG-3'
29	D2-1416	28/+	5'-GGAAATCAAAATAACACCACAGAGTTCC-3'
30	cD2-1503	34/-	5'-CTGCAGCAACACCATCTCATTGAAGTCGAGGCC-3'
31	D2-1510	25/+	5'-GACTTCAATGAGATGGTGCTGCTGC-3'
32	cD2-1510	25/+	5'-GCAGCAGCACCATCTCATTGAAGTC-3'
33	D2-1546	28/+	5'-AAGCTTGGCTGGTGACAGGCAATGGTT-3'
34	cD2-1567	27/-	5'-TGGTAACGGCAGGTCTAGGAACCATTG-3'
35	D2-1777	23/+	5'-GGACATCTCAAGTGCAGGCTGAG-3'
36	cD2-1777	23/+	5'-CTCAGCCTGCACTTGAGATGTCC-3'
37	D2-1863	27/+	5'-GAAGGAAATAGCAGAAACACAACATGG-3'
38	cD2-1888	33/-	5'-CCCTTCATATTGTACTCTGATAACTATTGTTCC-3'
39	D2-2047	32/+	5'-CCTCCATTCCGGAGACAGCTACATCATCATAGG-3'
40	cD2-2047	32/-	5'-CCTATGATGATGTAGCTGTCTCCGAATGGAGG-3'
41	D2-2170	29/+	5'-ATGGCCATTTTAGGTGACACAGCCTGGGA-3'
42	cD2-2200	27/-	5'-TGTAACACTCCTCCCAGGGATCCAAA-3'
43	D2-2308	29/+	5'-CTCATAGGAGTCATTATCATATGGATAGG-3'
44	cD2-2504	35/-	5'-GGGGATTCTGGTTGGAACCTATATTGTTCTGTCC-3'
45	cD2-2622	30/-	5'-TGATTCAATTCTGGTGTTATTTGTTTCCAC-3'
46	D2-2702	25/+	5'-AAGGAATCATGCAGGCAGGAAAACG-3'
47	cD2-2864	22/-	5'-ACTTCCAGCGAGTTCCAAGCTC-3'
			A A
48	D2-2992	25/+	5'-AACAGAGCCGTCCATGCCGATATGG-3'
49	cD2-3105	22/-	5'-TCCATTGCTCCAAAGGGTGTGT-3'
			G
50	D2-3236	25/+	5'-AGCTTGAGATGGACTTTGATTTCTG-3'

SEQ. ID			102
NO:	PRIMER	MER/SENSE	SEQUENCE
51	cD2-3410	22/-	5'-GGTCTGATTTCATCCCGTACC-3'
52	D2-3621	23/+	5'-GTCCTTTAGAGACCTGGGAAGAG-3'
53	cD2-3739	25/-	5'-GTTTTCTCAAGAGTAGTCCAGCTGC-3' C
54	D2-3905	25/+	5'-ATCAATTGGCAGTGACTATCATGGC-3'
55	cD2-4002	25/-	5'-TGTTAAGAGCAGTGGAGAAACGGAC-3' A G
56	cD2-4060	25/-	5'-GATTGAGACCTTTGATCGTCAACGC-3'
57	D2-4214	25/+	5'-TGACAGGACCATTAGTGGCTGGAGG-3'
58	D2-4257	34/+	5'-CGTGCTCACTGGACGATCGGCCGATTTGGAACG-3'
59	cD2-4323	24/-	5'-GGGCTGCTTCCTGATATTTCTGCC-3' C
60	D2-4497	25/+	5'-CCTGTGGGAAGTGAAGAAACAACGG-3'
61	cD2-4557	30/-	5'-GCTCCATCTTCCAGTTCAGCCTTTCCCATG-3'
62	cD2-4615	25/-	5'-CTCCGGCTCCAATCTGAGAGTATCC-3' G G A
63	D2-4746	25/+	5'-CCTAATATCATATGGAGGAGGCTGG-3'
64	D2-4792	25/+	5'-GAAGGAGAAGAAGTCCAGGTATTGG-3'
65	cD2-4922	25/-	5'-CTGTGCAACAATTGGAGATCCTGACG-3' T T
66	D2-4994	25/+	5'-GTGGAGCATATGTGAGTGCTATAGC-3'
67	D2-5124	25/+	5'-TCTGACTATGGCCGGAAGGTATCTC-3'
68	D2-5173	25/+	5'-ACATTAATCTTGGCCCCCACTAGAG-3'
69	cD2-5272	19/-	5'-CGATCTCCCGCCCGGTGTG-3' A
70	cD2-5318	25/-	5'-CTAACTGGTGATAGCAGCCTCATGG-3'
71	cD2-5656	27/-	5'-CCTACTGAGTTGTATCACTTTCTTTCC-3'
72	cD2-5891	26/-	5'-TGGATTCTTCCTATTCTCCCTCTTC-3'
73	D2-5770	25/+	5'-TTCAAGGCTGAGAGGGTTATAGACC-3'
74	D2-6152	25/+	5'-TCTGGTTGGCCTACAGAGTGGCAGC-3'
75	cD2-6252	27/-	5'-CCTTCTTTGTCCAGATTTCCACTTCC-3' A

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SEQ. ID	PRIMER	MER/SENSE	SEQUENCE
76	D2-6493	35/+	5'-GCGTACAACCATGCTCTCAGTGAAGTCCGGAGAC-3'
77	cD2-6605	24/-	5'-TTCCCAGGGTCATCTTCCCTATAC-3' G
78	cD2-6624	31/-	5'-GATGCTAGCCGTGATTATGCAGCACATTCCC-3'
79	D2-6748	25/+	5'-AAACAGAGAACACCCCCAAGACAACC-3'
80	cD2-6932	21/-	5'-CGGCATACAGCGTCCATGCTG-3'
81	D2-7055	25/+	5'-GTCTCGGGAAGGATGGCCATTGTC-3'
82	cD2-7195	25/-	5'-CTCTGGTTGCTTTTGCTTGAAGTCC-3' A G G
83	cD2-7217	27/-	5'-CCGCCGCTGCTCTTTTCTGAGCTTCTC-3'
84	D2-7378	25/+	5'-AGGACTACATGGGCTCTGTGTGAGG-3'
85	cD2-7515	19/-	5'-GAGAAGTCCAGCTCCGGCC-3'
86	D2-7769	25/+	5'-AGAGAAACATGGTCACACCAGAAGG-3'
87	cD2-7885	22/-	5'-GTTCTTCGTGTCCTGGTCCTCC-3'
88	D2-8165	25/+	5'-GGAAATATGGAGGAGCCTAGTGAGG-3'
89	cD2-8210	22/-	5'-ACCCAGTACATCTCATGTGTGG-3'
90	D2-8428	28/+	5'-GAGCATGAAACATCATGGCACTATGACC-3'
91	D2-8440	25/+	5'-TCATGGCACTATGACCAAGACCACC-3'
92	cD2-8529	22/-	5'-CAGTCTGACCACTCCGTTACC-3' C A G
93	D2-8773	25/+	5'-AAGGTGAGAAGCAATGCAGCCTTGG-3'
94	D2-8798	29/+	5'-GGGCCATATTTACTGATGAGAACAAGTGG-3'
95	cD2-8865	22/-	5'-TCTTTCCCTGTCAACCAGCTCC-3' C T
96	D2-9046	25/+	5'-AATGAAGATCACTGGTTCTCCAGAG-3'
97	D2-9131	25/+	5'-ACGTGAGCAAGAAAGAGGGAGGAGC-3'
98	cD2-9166	22/-	5'-TGTCCCATCCTGCTGTGTCATC-3' A G
99	cD2-9234	30/-	5'-GCTAGTTTCTTGTGTTCTCCTTCCATGTGG-3'
100	D2-9344	25/+	5'-TCATATCGAGAAGAGACCAAGAGG-3'
101	cD2-9429	24/-	5'-ACTCCTTCTCCCTCCATCTGTCTG-3'

SEQ. ID			104
NO:	PRIMER	MER/SENSE	SEQUENCE
102	cD2-9438	27/-	5'-ATGCTTTTGAAGATTCCTTCTCCCTCC-3' A C
103	cD2-9468	32/-	5'-GCACAGCGATTTCTTCTGTGATTGTTAGGTGC-3'
104	D2-9645	25/+	5'-ACAATGGGAACCTTCAAGAGGATGG-3'
105	D2-9656.BAM	45/+	5'-TTATCACATT/GGATCC/TTCAAGAGGATGGA ATGATTGGACACAAG-3' (5'-Fill/BamHI/DEN-2 Sequence)
106	cD2-9668	28/-	5'-CAGAAGGGCACTTGTGTCCAATCATTCC-3'
107	cD2-9779	21/-	5'-CTCCCTGGGAAATTCGGGGCTC-3' T G
108	cD2-9796	28/-	5'-CCGTCTCCCGCAAAGACCACCCTGCTCC-3'
109	cD2-9796.XBA	44/-	5'-TTATCACCTA/TCTAGA/CCGTCTCCC GCAAAGACCACCCTGCTCC-3'
110	cD2-9913	26/-	5'-GTTGGAACCCAATGTGATGGTACTGC-3'
111	D2-9937	25/+	5'-ACAAGTCGAACAACCTGGTCCATAC-3'
112	cD2-9977	21/-	5'-GCATGTCTTCCGTCTGTCATCC-3' T
113	cD2-10003	25/-	5'-CTTGAATCCACACCCTGTTCCAGAC-3'
114	D2-10203	25/+	5'-ATACACAGATTACATGCCATCCATG-3'
115	cD2-10261	21/-	5'-TTTTGCCTTCTACCACAGGAC-3' T A
116	D2-10289	25/-	5'-GAAACAAGGCTAGAAGTCAGGTCGG-3'
117	cD2-10337	23/-	5'-GACGGGGCTCACAGGTAGCATAG-3'
118	D2-10418	25/+	5'-GCCTGTAGCTCCACCTGAGAAGGTG-3'
119	D2-10470	25/+	5'-GGAAGCTGTACGCATGGCGTAGTGG-3'
120	cD2-10530	19/-	5'-GGGCCCCCGTTGTTGCTGC-3' A
121	cD2-10687	59/-	5'-AGAACCTGTTGATTCAACAGCACCATTCCATTTCTG-3'
122	cD2-10687.XBA	59/-	5'-TTATCACCTA/GCATGC/TCTAGA/ AGAACCTGTTGATTCAACAGCACCATTCCATTTCTG-3' (5'-Fill/SphI/XbaI/ 3'-End DEN-2 Sequence)
123	cD2-10687.X2	52/-	5'-TTATCACCTA/TCTAGA/ GAACCTGTTGATTCAACAGCACCATTCCATTTCTG-3' (5'-Fill/XbaI/ 3'-End DEN-2 Sequence)

While particular embodiments of the invention have been described in detail, it will be apparent to those skilled in the art that these embodiments are exemplary rather than limiting, and the true scope of the invention is that defined within the attached claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: MAHIDOL UNIVERSITY
Bangkok, Thailand

The United States of
America, as represented by the Secretary,
Department of Health and Human Services
c/o Centers for Disease Control and
Prevention
Technology Transfer Office
Mail Stop E-67
1600 Clifton Road
Atlanta, Georgia 30333

(ii) TITLE OF THE INVENTION: INFECTIOUS CDNA CLONES FOR DENGUE 2
VIRUS ...

(iii) NUMBER OF SEQUENCES: 137

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: NEEDLE & ROSENBERG, P.C.
(B) STREET: Suite 1200, 127 Peachtree Street, NE
(C) CITY: Atlanta
(D) STATE: GA
(E) COUNTRY: USA
(F) ZIP: 30303

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: U.S. Serial No. 08/483,292
(B) FILING DATE: 7 Jun 1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Spratt, Gwendolyn D.
(B) REGISTRATION NUMBER: 36,016
(C) REFERENCE/DOCKET NUMBER: 14114.0179/P

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 404-688-0770
(B) TELEFAX: 404-688-9880
(C) TELEX:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 97...10269

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGTTGTTAGT CTACGTGGAC CGACAAAGAC AGATTCTTTG AGGGAGCTAA GCTCAACGTA	60
GTTCTAACAG TTTTSTAATT AGAGAGCAGA TCTCTG ATG AAT AAC CAA CGG AAA	114
Met Asn Asn Gln Arg Lys	
1 5	
AAG GCG AAA AAC ACG CCT TTC AAT ATG CTG AAA CGC GAG AGA AAC CGC	162
Lys Ala Lys Asn Thr Pro Phe Asn Met Leu Lys Arg Glu Arg Asn Arg	
10 15 20	
GTG TCG ACT GTG CAA CAG CTG ACA AAG AGA TTC TCA CTT GGA ATG CTG	210
Val Ser Thr Val Gln Gln Leu Thr Lys Arg Phe Ser Leu Gly Met Leu	
25 30 35	
CAG GGA CGA GGA CCA TTA AAA CTG TTC ATG GCC CTG GTG GCG TTC CTT	258
Gln Gly Arg Gly Pro Leu Lys Leu Phe Met Ala Leu Val Ala Phe Leu	
40 45 50	
CGT TTC CTA ACA ATC CCA CCA ACA GCA GGG ATA TTG AAG AGA TGG GGA	306
Arg Phe Leu Thr Ile Pro Pro Thr Ala Gly Ile Leu Lys Arg Trp Gly	
55 60 65 70	
ACA ATT AAA AAA TCA AAA GCT ATT AAT GTT TTG AGA GGG TTC AGG AAA	354
Thr Ile Lys Lys Ser Lys Ala Ile Asn Val Leu Arg Gly Phe Arg Lys	
75 80 85	
GAG ATT GGA AGG ATG CTG AAC ATC TTG AAT AGG AGA CGC AGA TCT GCA	402
Glu Ile Gly Arg Met Leu Asn Ile Leu Asn Arg Arg Arg Arg Ser Ala	
90 95 100	
GGC ATG ATC ATT ATG CTG ATT CCA ACA GTG ATG GCG TTC CAT TTA ACC	450
Gly Met Ile Ile Met Leu Ile Pro Thr Val Met Ala Phe His Leu Thr	
105 110 115	
ACA CGT AAC GGA GAA CCA CAC ATG ATC GTC AGC AGA CAA GAG AAA GGG	498
Thr Arg Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly	
120 125 130	

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AAA Lys 135	AGT Ser	CTT Leu	CTG Leu	TTT Phe	AAA Lys 140	ACA Thr	GAG Glu	GAT Asp	GGC Gly	GTG Val 145	AAC Asn	ATG Met	TGT Cys	ACC Thr	CTC Leu 150	546
ATG Met	GCC Ala	ATG Met	GAC Asp	CTT Leu 155	GGT Gly	GAA Glu	TTG Leu	TGT Cys	GAA Glu 160	GAC Asp	ACA Thr	ATC Ile	ACG Thr	TAC Tyr 165	AAG Lys	594
TGT Cys	CCC Pro	CTT Leu	CTC Leu 170	AGG Arg	CAG Gln	AAT Asn	GAG Glu	CCA Pro 175	GAA Glu	GAC Asp	ATA Ile	GAC Asp	TGT Cys 180	TGG Trp	TGC Cys	642
AAC Asn	TCT Ser 185	ACG Thr	TCC Ser	ACG Thr	TGG Trp	GTA Val	ACT Thr 190	TAT Tyr	GGG Gly	ACG Thr	TGT Cys 195	ACC Thr	ACC Thr	ATG Met	GGA Gly	690
GAA Glu 200	CAT His	AGA Arg	AGA Arg	GAA Glu	AAA Lys 205	AGA Arg	TCA Ser	GTG Val	GCA Ala	CTC Leu 210	GTT Val	CCA Pro	CAT His	GTG Val	GGA Gly	738
ATG Met 215	GGA Gly	CTG Leu	GAG Glu	ACA Thr	CGA Arg 220	ACT Thr	GAA Glu	ACA Thr	TGG Trp	ATG Met 225	TCA Ser	TCA Ser	GAA Glu	GGG Gly	GCC Ala 230	786
TGG Trp	AAA Lys	CAT His	GTC Val	CAG Gln 235	AGA Arg	ATT Ile	GAA Glu	ACT Thr 240	TGG Trp	ATC Ile	TTG Leu	AGA Arg	CAT His 245	CCA Pro	GGC Gly	834
TTC Phe	ACC Thr	ATG Met	ATG Met 250	GCA Ala	GCA Ala	ATC Ile	CTG Leu 255	GCA Ala	TAC Tyr	ACC Thr	ATA Ile	GGA Gly	ACG Thr 260	ACA Thr	CAT His	882
TTC Phe	CAA Gln 265	AGA Arg	GCC Ala	CTG Leu	ATT Ile	TTC Phe 270	ATC Ile	TTA Leu	CTG Leu	ACA Thr	GCT Ala 275	GTC Val	ACT Thr	CCT Pro	TCA Ser	930
ATG Met 280	ACA Thr	ATG Met	CGT Arg	TGC Cys	ATA Ile 285	GGA Gly	ATG Met	TCA Ser	AAT Asn	AGA Arg	GAC Asp 290	TTT Phe	GTG Val	GAA Glu	GGG Gly	978
GTT Val 295	TCA Ser	GGA Gly	GGA Gly	AGC Ser	TGG Trp 300	GTT Val	GAC Asp	ATA Ile	GTC Val 305	TTA Leu	GAA Glu	CAT His	GGA Gly	AGC Ser	TGT Cys 310	1026
GTG Val	ACG Thr	ACG Thr	ATG Met	GCA Ala 315	AAA Lys	AAC Asn	AAA Lys	CCA Pro	ACA Thr 320	TTG Leu	GAT Asp	TTT Phe	GAA Glu	CTG Leu 325	ATA Ile	1074
AAA Lys	ACA Thr	GAA Glu	GCC Ala 330	AAA Lys	CAG Gln	CCT Pro	GCC Ala	ACC Thr 335	CTA Leu	AGG Arg	AAG Lys	TAC Tyr	TGT Cys 340	ATA Ile	GAG Glu	1122
GCA Ala	AAG Lys	CTA Leu 345	ACC Thr	AAC Asn	ACA Thr	ACA Thr	ACA Thr 350	GAA Glu	TCT Ser	CGC Arg	TGC Cys	CCA Pro 355	ACA Thr	CAA Gln	GGG Gly	1170

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GAA CCC AGC CTA AAT GAA GAG CAG GAC AAA AGG TTC GTC TGC AAA CAC Glu Pro Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His 360 365 370	1218
TCC ATG GTA GAC AGA GGA TGG GGA AAT GGA TGT GGA CTA TTT GGA AAG Ser Met Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys 375 380 385 390	1266
GGA GGC ATT GTG ACC TGT GCT ATG TTC AGA TGC AAA AAG AAC ATG GAA Gly Gly Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu 395 400 405	1314
GGA AAA GTT GTG CAA CCA GAA AAC TTG GAA TAC ACC ATT GTG ATA ACA Gly Lys Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr 410 415 420	1362
CCT CAC TCA GGG GAA GAG CAT GCA GTC GGA AAT GAC ACA GGA AAA CAT Pro His Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His 425 430 435	1410
GGC AAG GAA ATC AAA ATA ACA CCA CAG AGT TCC ATC ACA GAA GCA GAA Gly Lys Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu 440 445 450	1458
TTG ACA GGT TAT GGC ACT GTC ACA ATG GAG TGC TCT CCA AGA ACG GGC Leu Thr Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly 455 460 465 470	1506
CTC GAC TTC AAT GAG ATG GTG TTG CTG CAG ATG GAA AAT AAA GCT TGG Leu Asp Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp 475 480 485	1554
CTG GTG CAC AGG CAA TGG TTC CTA GAC CTG CCG TTA CCA TGG TTG CCC Leu Val His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro 490 495 500	1602
GGA GCG GAC ACA CAA GGG TCA AAT TGG ATA CAG AAA GAG ACA TTG GTC Gly Ala Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val 505 510 515	1650
ACT TTC AAA AAT CCC CAT GCG AAG AAA CAG GAT GTT GTT GTT TTA GGA Thr Phe Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly 520 525 530	1698
TCC CAA GAA GGG GCC ATG CAC ACA GCA CTT ACA GGG GCC ACA GAA ATC Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile 535 540 545 550	1746
CAA ATG TCA TCA GGA AAC TTA CTC TTC ACA GGA CAT CTC AAG TGC AGG Gln Met Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg 555 560 565	1794
CTG AGA ATG GAC AAG CTA CAG CTC AAA GGA ATG TCA TAC TCT ATG TGC Leu Arg Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys 570 575 580	1842
ACA GGA AAG TTT AAA GTT GTG AAG GAA ATA GCA GAA ACA CAA CAT GGA Thr Gly Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly 585 590 595	1890

1:10

ACA Thr 600	ATA Ile	GTT Val	ATC Ile	AGA Arg	GTG Val	CAA Gln 605	TAT Tyr	GAA Glu	GGG Gly	GAC Asp	GGC Gly 610	TCT Ser	CCA Pro	TGC Cys	AAG Lys	1938
ATC Ile 615	CCT Pro	TTT Phe	GAG Glu	ATA Ile	ATG Met 620	GAT Asp	TTG Leu	GAA Glu	AAA Lys	AGA Arg 625	CAT His	GTC Val	TTA Leu	GGT Gly	CGC Arg 630	1986
CTG Leu	ATT Ile	ACA Thr	GTC Val	AAC Asn 635	CCA Pro	ATT Ile	GTG Val	ACA Thr	GAA Glu 640	AAA Lys	GAT Asp	AGC Ser	CCA Pro	GTC Val 645	AAC Asn	2034
ATA Ile	GAA Glu	GCA Ala	GAA Glu 650	CCT Pro	CCA Pro	TTC Phe	GGA Gly	GAC Asp 655	AGC Ser	TAC Tyr	ATC Ile	ATC Ile	ATA Ile 660	GGA Gly	GTA Val	2082
GAG Glu	CCG Pro	GGA Gly 665	CAA Gln	CTG Leu	AAG Lys	CTC Leu	AAC Asn 670	TGG Trp	TTT Phe	AAG Lys	AAA Lys	GGA Gly 675	AGT Ser	TCT Ser	ATC Ile	2130
GGC Gly 680	CAA Gln	ATG Met	TTT Phe	GAG Glu	ACA Thr	ACA Thr 685	ATG Met	AGG Arg	GGG Gly	GCG Ala	AAG Lys 690	AGA Arg	ATG Met	GCC Ala	ATT Ile	2178
TTA Leu 695	GGT Gly	GAC Asp	ACA Thr	GCC Ala	TGG Trp 700	GAT Asp	TTT Phe	GGA Gly	TCC Ser	TTG Leu 705	GGA Gly	GGA Gly	GTG Val	TTT Phe	ACA Thr 710	2226
TCT Ser	ATA Ile	GGA Gly	AAG Lys	GCT Ala 715	CTC Leu	CAC His	CAA Gln	GTC Val	TTT Phe 720	GGA Gly	GCA Ala	ATC Ile	TAT Tyr	GGA Gly 725	GCT Ala	2274
GCC Ala	TTC Phe	AGT Ser	GGG Gly 730	GTT Val	TCA Ser	TGG Trp	ACT Thr	ATG Met 735	AAA Lys	ATC Ile	CTC Leu	ATA Ile	GGA Gly 740	GTC Val	ATT Ile	2322
ATC Ile	ACA Thr	TGG Trp 745	ATA Ile	GGA Gly	ATG Met	AAT Asn	TCA Ser 750	CGC Arg	AGC Ser	ACC Thr	TCA Ser	CTG Leu	TCT Ser	GTG Val	ACA Thr	2370
CTA Leu 760	GTA Val	TTG Leu	GTG Val	GGA Gly	ATT Ile	GTG Val 765	ACA Thr	CTG Leu	TAT Tyr	TTG Leu 770	GGA Gly	GTC Val	ATG Met	GTG Val	CAG Gln	2418
GCC Ala 775	GAT Asp	AGT Ser	GGT Gly	TGC Cys	GTT Val 780	GTG Val	AGC Ser	TGG Trp	AAA Lys	AAC Asn 785	AAA Lys	GAA Glu	CTG Leu	AAA Lys	TGT Cys 790	2466
GGC Gly	AGT Ser	GGG Gly	ATT Ile	TTC Phe 795	ATC Ile	ACA Thr	GAC Asp	AAC Asn	GTG Val 800	CAC His	ACA Thr	TGG Trp	ACA Thr	GAA Glu 805	CAA Gln	2514
TAC Tyr	AAG Lys	TTC Phe	CAA Gln 810	CCA Pro	GAA Glu	TCC Ser	CCT Pro	TCA Ser 815	AAA Lys	CTA Leu	GCT Ala	TCA Ser	GCT Ala 820	ATC Ile	CAG Gln	2562
AAA Lys	GCC Ala	CAT His 825	GAA Glu	GAG Glu	GGC Gly	ATT Ile	TGT Cys 830	GGA Gly	ATC Ile	CGC Arg	TCA Ser	GTA Val 835	ACA Thr	AGA Arg	CTG Leu	2610

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GAG AAT CTG ATG TGG AAA CAA ATA ACA CCA GAA TTG AAT CAC ATT CTA Glu Asn Leu Met Trp Lys Gln Ile Thr Pro Glu Leu Asn His Ile Leu 840 845 850	2658
TCA GAA AAT GAG GTG AAG TTA ACT ATT ATG ACA GGA GAC ATC AAA GGA Ser Glu Asn Glu Val Lys Leu Thr Ile Met Thr Gly Asp Ile Lys Gly 855 860 865 870	2706
ATC ATG CAG GCA GGA AAA CGA TCT CTG CGG CCT CAG CCC ACT GAG CTG Ile Met Gln Ala Gly Lys Arg Ser Leu Arg Pro Gln Pro Thr Glu Leu 875 880 885	2754
AAG TAT TCA TGG AAA ACA TGG GGC AAA GCA AAA ATG CTC TCT ACA GAG Lys Tyr Ser Trp Lys Thr Trp Gly Lys Ala Lys Met Leu Ser Thr Glu 890 895 900	2802
TCT CAT AAC CAG ACC TTT CTC ATT GAT GGC CCC GAA ACA GCA GAA TGC Ser His Asn Gln Thr Phe Leu Ile Asp Gly Pro Glu Thr Ala Glu Cys 905 910 915	2850
CCC AAC ACA AAT AGA GCT TGG AAT TCG TTG GAA GTT GAA GAC TAT GGC Pro Asn Thr Asn Arg Ala Trp Asn Ser Leu Glu Val Glu Asp Tyr Gly 920 925 930	2898
TTT GGA GTA TTC ACC ACC AAT ATA TGG CTA AAA TTG AAA GAA AAA CAG Phe Gly Val Phe Thr Thr Asn Ile Trp Leu Lys Leu Lys Glu Lys Gln 935 940 945 950	2946
GAT GTA TTC TGC GAC TCA AAA CTC ATG TCA GCG GCC ATA AAA GAC AAC Asp Val Phe Cys Asp Ser Lys Leu Met Ser Ala Ala Ile Lys Asp Asn 955 960 965	2994
AGA GCC GTC CAT GCC GAT ATG GGT TAT TGG ATA GAA AGT GCA CTC AAT Arg Ala Val His Ala Asp Met Gly Tyr Trp Ile Glu Ser Ala Leu Asn 970 975 980	3042
GAC ACA TGG AAG ATA GAG AAA GCC TCT TTC ATT GAA GTT AAA AAC TGC Asp Thr Trp Lys Ile Glu Lys Ala Ser Phe Ile Glu Val Lys Asn Cys 985 990 995	3090
CAC TGG CCA AAA TCA CAC ACC CTC TGG AGC AAT GGA GTG CTA GAA AGT His Trp Pro Lys Ser His Thr Leu Trp Ser Asn Gly Val Leu Glu Ser 1000 1005 1010	3138
GAG ATG ATA ATT CCA AAG AAT CTC GCT GGA CCA GTG TCT CAA CAC AAC Glu Met Ile Ile Pro Lys Asn Leu Ala Gly Pro Val Ser Gln His Asn 1015 1020 1025 1030	3186
TAT AGA CCA GGC TAC CAT ACA CAA ATA ACA GGA CCA TGG CAT CTA GGT Tyr Arg Pro Gly Tyr His Thr Gln Ile Thr Gly Pro Trp His Leu Gly 1035 1040 1045	3234
AAG CTT GAG ATG GAC TTT GAT TTC TGT GAT GGA ACA ACA GTG GTA GTG Lys Leu Glu Met Asp Phe Asp Phe Cys Asp Gly Thr Thr Val Val Val 1050 1055 1060	3282
ACT GAG GAC TGC GGA AAT AGA GGA CCC TCT TTG AGA ACA ACC ACT GCC Thr Glu Asp Cys Gly Asn Arg Gly Pro Ser Leu Arg Thr Thr Thr Ala 1065 1070 1075	3330

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TCT GGA AAA CTC ATA ACA GAA TGG TGC TGC CGA TCT TGC ACA TTA CCA	3378
Ser Gly Lys Leu Ile Thr Glu Trp Cys Cys Arg Ser Cys Thr Leu Pro	
1080 1085 1090	
CCG CTA AGA TAC AGA GGT GAG GAT GGG TGC TGG TAC GGG ATG GAA ATC	3426
Pro Leu Arg Tyr Arg Gly Glu Asp Gly Cys Trp Tyr Gly Met Glu Ile	
1095 1100 1105 1110	
AGA CCA TTG AAG GAG AAA GAA GAG AAT TTG GTC AAC TCC TTG GTC ACA	3474
Arg Pro Leu Lys Glu Lys Glu Glu Asn Leu Val Asn Ser Leu Val Thr	
1115 1120 1125	
GCT GGA CAT GGG CAG GTC GAC AAC TTT TCA CTA GGA GTC TTG GGA ATG	3522
Ala Gly His Gly Gln Val Asp Asn Phe Ser Leu Gly Val Leu Gly Met	
1130 1135 1140	
GCA TTG TTC CTG GAG GAA ATG CTT AGG ACC CGA GTA GGA ACG AAA CAT	3570
Ala Leu Phe Leu Glu Glu Met Leu Arg Thr Arg Val Gly Thr Lys His	
1145 1150 1155	
GCA ATA CTA CTA GTT GCA GTT TCT TTT GTG ACA TTG ATC ACA GGG AAC	3618
Ala Ile Leu Leu Val Ala Val Ser Phe Val Thr Leu Ile Thr Gly Asn	
1160 1165 1170	
ATG TCC TTT AGA GAC CTG GGA AGA GTG ATG GTT ATG GTA GGC GCC ACT	3666
Met Ser Phe Arg Asp Leu Gly Arg Val Met Val Met Val Gly Ala Thr	
1175 1180 1185 1190	
ATG ACG GAT GAC ATA GGT ATG GGC GTG ACT TAT CTT GCC CTA CTA GCA	3714
Met Thr Asp Asp Ile Gly Met Gly Val Thr Tyr Leu Ala Leu Leu Ala	
1195 1200 1205	
GCC TTC AAA GTC AGA CCA ACT TTT GCA GCT GGA CTA CTC TTG AGA AAG	3762
Ala Phe Lys Val Arg Pro Thr Phe Ala Ala Gly Leu Leu Leu Arg Lys	
1210 1215 1220	
CTG ACC TCC AAG GAA TTG ATG ATG ACT ACT ATA GGA ATT GTA CTC CTC	3810
Leu Thr Ser Lys Glu Leu Met Met Thr Thr Ile Gly Ile Val Leu Leu	
1225 1230 1235	
TCC CAG AGC ACC ATA CCA GAG ACC ATT CTT GAG TTG ACT GAT GCG TTA	3858
Ser Gln Ser Thr Ile Pro Glu Thr Ile Leu Glu Leu Thr Asp Ala Leu	
1240 1245 1250	
GCC TTA GGC ATG ATG GTC CTC AAA ATG GTG AGA AAT ATG GAA AAG TAT	3906
Ala Leu Gly Met Met Val Leu Lys Met Val Arg Asn Met Glu Lys Tyr	
1255 1260 1265 1270	
CAA TTG GCA GTG ACT ATC ATG GCT ATC TTG TGC GTC CCA AAC GCA GTG	3954
Gln Leu Ala Val Thr Ile Met Ala Ile Leu Cys Val Pro Asn Ala Val	
1275 1280 1285	
ATA TTA CAA AAC GCA TGG AAA GTG AGT TGC ACA ATA TTG GCA GTG GTG	4002
Ile Leu Gln Asn Ala Trp Lys Val Ser Cys Thr Ile Leu Ala Val Val	
1290 1295 1300	
TCC GTT TCC CCA CTG CTC TTA ACA TCC TCA CAG CAA AAA ACA GAT TGG	4050
Ser Val Ser Pro Leu Leu Leu Thr Ser Ser Gln Gln Lys Thr Asp Trp	
1305 1310 1315	

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ATA CCA TTA GCA TTG ACG ATC AAA GGT CTC AAT CCA ACA GCT ATT TTT Ile Pro Leu Ala Leu Thr Ile Lys Gly Leu Asn Pro Thr Ala Ile Phe 1320 1325 1330	4098
CTA ACA ACC CTC TCA AGA ACC AGC AAG AAA AGG AGC TGG CCA TTA AAT Leu Thr Thr Leu Ser Arg Thr Ser Lys Lys Arg Ser Trp Pro Leu Asn 1335 1340 1345 1350	4146
GAG GCT ATC ATG GCA GTC GGG ATG GTG AGC ATT TTA GCC AGT TCT CTC Glu Ala Ile Met Ala Val Gly Met Val Ser Ile Leu Ala Ser Ser Leu 1355 1360 1365	4194
CTA AAA AAT GAT ATT CCC ATG ACA GGA CCA TTA GTG GCT GGA GGG CTC Leu Lys Asn Asp Ile Pro Met Thr Gly Pro Leu Val Ala Gly Gly Leu 1370 1375 1380	4242
CTC ACT GTG TGC TAC GTG CTC ACT GGA CGA TCG GCC GAT TTG GAA CTG Leu Thr Val Cys Tyr Val Leu Thr Gly Arg Ser Ala Asp Leu Glu Leu 1385 1390 1395	4290
GAG AGA GCA GCC GAT GTC AAA TGG GAA GAC CAG GCA GAG ATA TCA GGA Glu Arg Ala Ala Asp Val Lys Trp Glu Asp Gln Ala Glu Ile Ser Gly 1400 1405 1410	4338
AGC AGT CCA ATC CTG TCA ATA ACA ATA TCA GAA GAT GGT AGC ATG TCG Ser Ser Pro Ile Leu Ser Ile Thr Ile Ser Glu Asp Gly Ser Met Ser 1415 1420 1425 1430	4386
ATA AAA AAT GAA GAG GAA GAA CAA ACA CTG ACC ATA CTC ATT AGA ACA Ile Lys Asn Glu Glu Glu Glu Gln Thr Leu Thr Ile Leu Ile Arg Thr 1435 1440 1445	4434
GGA TTG CTG GTG ATC TCA GGA CTT TTT CCT GTA TCA ATA CCA ATC ACG Gly Leu Leu Val Ile Ser Gly Leu Phe Pro Val Ser Ile Pro Ile Thr 1450 1455 1460	4482
GCA GCA GCA TGG TAC CTG TGG GAA GTG AAG AAA CAA CGG GCC GGA GTA Ala Ala Ala Trp Tyr Leu Trp Glu Val Lys Lys Gln Arg Ala Gly Val 1465 1470 1475	4530
TTG TGG GAT GTT CCT TCA CCC CCA CCC ATG GGA AAG GCT GAA CTG GAA Leu Trp Asp Val Pro Ser Pro Pro Met Gly Lys Ala Glu Leu Glu 1480 1485 1490	4578
GAT GGA GCC TAT AGA ATT AAG CAA AAA GGG ATT CTT GGA TAT TCC CAG Asp Gly Ala Tyr Arg Ile Lys Gln Lys Gly Ile Leu Gly Tyr Ser Gln 1495 1500 1505 1510	4626
ATC GGA GCC GGA GTT TAC AAA GAA GGA ACA TTC CAT ACA ATG TGG CAT Ile Gly Ala Gly Val Tyr Lys Glu Gly Thr Phe His Thr Met Trp His 1515 1520 1525	4674
GTC ACA CGT GGC GCT GTT CTA ATG CAT AAA GGA AAG AGG ATT GAA CCA Val Thr Arg Gly Ala Val Leu Met His Lys Gly Lys Arg Ile Glu Pro 1530 1535 1540	4722
TCA TGG GCG GAC GTC AAG AAA GAC CTA ATA TCA TAT GGA GGA GGC TGG Ser Trp Ala Asp Val Lys Lys Asp Leu Ile Ser Tyr Gly Gly Gly Trp 1545 1550 1555	4770

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AAG TTA GAA GGA GAA TGG AAG GAA GGA GAA GAA GTC CAG GTA TTG GCA Lys Leu Glu Gly Glu Trp Lys Glu Gly Glu Glu Val Gln Val Leu Ala 1560 1565 1570	4818
CTG GAG CCT GGA AAA AAT CCA AGA GCC GTC CAA ACG AAA CCT GGT CTT Leu Glu Pro Gly Lys Asn Pro Arg Ala Val Gln Thr Lys Pro Gly Leu 1575 1580 1585 1590	4866
TTC AAA ACC AAC GCC GGA ACA ATA GGT GCT GTA TCT CTG GAC TTT TCT Phe Lys Thr Asn Ala Gly Thr Ile Gly Ala Val Ser Leu Asp Phe Ser 1595 1600 1605	4914
CCT GGA ACG TCA GGA TCT CCA ATT ATC GAC AAA AAA GGA AAA GTT GTG Pro Gly Thr Ser Gly Ser Pro Ile Ile Asp Lys Lys Gly Lys Val Val 1610 1615 1620	4962
GGT CTT TAT GGT AAT GGT GTT GTT ACA AGG AGT GGA GCA TAT GTG AGT Gly Leu Tyr Gly Asn Gly Val Val Thr Arg Ser Gly Ala Tyr Val Ser 1625 1630 1635	5010
GCT ATA GCC CAG ACT GAA AAA AGC ATT GAA GAC AAC CCA GAG ATC GAA Ala Ile Ala Gln Thr Glu Lys Ser Ile Glu Asp Asn Pro Glu Ile Glu 1640 1645 1650	5058
GAT GAC ATT TTC CGA AAG AGA AGA CTG ACC ATC ATG GAC CTC CAC CCA Asp Asp Ile Phe Arg Lys Arg Arg Leu Thr Ile Met Asp Leu His Pro 1655 1660 1665 1670	5106
GGA GCG GGA AAG ACG AAG AGA TAC CTT CCG GCC ATA GTC AGA GAA GCT Gly Ala Gly Lys Thr Lys Arg Tyr Leu Pro Ala Ile Val Arg Glu Ala 1675 1680 1685	5154
ATA AAA CGG GGT TTG AGA ACA TTA ATC TTG GCC CCC ACT AGA GTT GTG Ile Lys Arg Gly Leu Arg Thr Leu Ile Leu Ala Pro Thr Arg Val Val 1690 1695 1700	5202
GCA GCT GAA ATG GAG GAA GCC CTT AGA GGA CTT CCA ATA AGA TAC CAG Ala Ala Glu Met Glu Glu Ala Leu Arg Gly Leu Pro Ile Arg Tyr Gln 1705 1710 1715	5250
ACC CCA GCC ATC AGA GCT GAG CAC ACC GGG CGG GAG ATT GTG GAC CTA Thr Pro Ala Ile Arg Ala Glu His Thr Gly Arg Glu Ile Val Asp Leu 1720 1725 1730	5298
ATG TGT CAT GCC ACA TTT ACC ATG AGG CTG CTA TCA CCA GTT AGA GTG Met Cys His Ala Thr Phe Thr Met Arg Leu Leu Ser Pro Val Arg Val 1735 1740 1745 1750	5346
CCA AAC TAC AAC CTG ATT ATC ATG GAC GAA GCC CAT TTC ACA GAC CCA Pro Asn Tyr Asn Leu Ile Ile Met Asp Glu Ala His Phe Thr Asp Pro 1755 1760 1765	5394
GCA AGT ATA GCA GCT AGA GGA TAC ATC TCA ACT CGA GTG GAG ATG GGT Ala Ser Ile Ala Ala Arg Gly Tyr Ile Ser Thr Arg Val Glu Met Gly 1770 1775 1780	5442
GAG GCA GCT GGG ATT TTT ATG ACA GCC ACT CCC CCG GGA AGC AGA GAC Glu Ala Ala Gly Ile Phe Met Thr Ala Thr Pro Pro Gly Ser Arg Asp 1785 1790 1795	5490

115.

CCA TTT CCT CAG AGC AAT GCA CCA ATC ATA GAT GAA GAA AGA GAA ATC Pro Phe Pro Gln Ser Asn Ala Pro Ile Ile Asp Glu Glu Arg Glu Ile 1800 1805 1810	5538
CCT GAA CGC TCG TGG AAT TCC GGA CAT GAA TGG GTC ACG GAT TTT AAA Pro Glu Arg Ser Trp Asn Ser Gly His Glu Trp Val Thr Asp Phe Lys 1815 1820 1825 1830	5586
GGG AAG ACT GTT TGG TTC GTT CCA AGT ATA AAA GCA GGA AAT GAT ATA Gly Lys Thr Val Trp Phe Val Pro Ser Ile Lys Ala Gly Asn Asp Ile 1835 1840 1845	5634
GCA GCT TGC CTG AGG AAA AAT GGA AAG AAA GTG ATA CAA CTC AGT AGG Ala Ala Cys Leu Arg Lys Asn Gly Lys Lys Val Ile Gln Leu Ser Arg 1850 1855 1860	5682
AAG ACC TTT GAT TCT GAG TAT GTC AAG ACT AGA ACC AAT GAT TGG GAC Lys Thr Phe Asp Ser Glu Tyr Val Lys Thr Arg Thr Asn Asp Trp Asp 1865 1870 1875	5730
TTC GTG GTT ACA ACT GAC ATT TCA GAA ATG GGT GCC AAT TTC AAG GCT Phe Val Val Thr Thr Asp Ile Ser Glu Met Gly Ala Asn Phe Lys Ala 1880 1885 1890	5778
GAG AGG GTT ATA GAC CCC AGA CGC TGC ATG AAA CCA GTC ATA CTA ACA Glu Arg Val Ile Asp Pro Arg Arg Cys Met Lys Pro Val Ile Leu Thr 1895 1900 1905 1910	5826
GAT GGT GAA GAG CGG GTG ATT CTG GCA GGA CCT ATG CCA GTG ACC CAC Asp Gly Glu Glu Arg Val Ile Leu Ala Gly Pro Met Pro Val Thr His 1915 1920 1925	5874
TCT AGT GCA GCA CAA AGA AGA GGG AGA ATA GGA AGA AAT CCA AAA AAT Ser Ser Ala Ala Gln Arg Arg Gly Arg Ile Gly Arg Asn Pro Lys Asn 1930 1935 1940	5922
GAG AAT GAC CAG TAC ATA TAC ATG GGG GAA CCT CTG GAA AAT GAT GAA Glu Asn Asp Gln Tyr Ile Tyr Met Gly Glu Pro Leu Glu Asn Asp Glu 1945 1950 1955	5970
GAC TGT GCA CAC TGG AAA GAA GCT AAA ATG CTC CTA GAT AAC ATC AAC Asp Cys Ala His Trp Lys Glu Ala Lys Met Leu Leu Asp Asn Ile Asn 1960 1965 1970	6018
ACG CCA GAA GGA ATC ATT CCT AGC ATG TTC GAA CCA GAG CGT GAA AAG Thr Pro Glu Gly Ile Ile Pro Ser Met Phe Glu Pro Glu Arg Glu Lys 1975 1980 1985 1990	6066
GTG GAT GCC ATT GAT GGC GAA TAC CGC TTG AGA GGA GAA GCA AGG AAA Val Asp Ala Ile Asp Gly Glu Tyr Arg Leu Arg Gly Glu Ala Arg Lys 1995 2000 2005	6114
ACC TTT GTA GAC TTA ATG AGA AGA GGA GAC CTA CCA GTC TGG TTG GCC Thr Phe Val Asp Leu Met Arg Arg Gly Asp Leu Pro Val Trp Leu Ala 2010 2015 2020	6162
TAC AGA GTG GCA GCT GAA GGC ATC AAC TAC GCA GAC AGA AGG TGG TGT Tyr Arg Val Ala Ala Glu Gly Ile Asn Tyr Ala Asp Arg Arg Trp Cys 2025 2030 2035	6210

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TTT GAT GGA GTC AAG AAC AAC CAA ATC CTA GAA GAA AAC GTG GAA GTT Phe Asp Gly Val Lys Asn Asn Gln Ile Leu Glu Glu Asn Val Glu Val 2040 2045 2050	6258
GAA ATC TGG ACA AAA GAA GGG GAA AGG AAG AAA TTG AAA CCC AGA TGG Glu Ile Trp Thr Lys Glu Gly Glu Arg Lys Lys Leu Lys Pro Arg Trp 2055 2060 2065 2070	6306
TTG GAT GCT AGG ATC TAT TCT GAC CCA CTG GCG CTA AAA GAA TTT AAG Leu Asp Ala Arg Ile Tyr Ser Asp Pro Leu Ala Leu Lys Glu Phe Lys 2075 2080 2085	6354
GAA TTT GCA GCC GGA AGA AAG TCT CTG ACC CTG AAC CTA ATC ACA GAA Glu Phe Ala Ala Gly Arg Lys Ser Leu Thr Leu Asn Leu Ile Thr Glu 2090 2095 2100	6402
ATG GGT AGG CTC CCA ACC TTC ATG ACT CAG AAG GCA AGA GAC GCA CTG Met Gly Arg Leu Pro Thr Phe Met Thr Gln Lys Ala Arg Asp Ala Leu 2105 2110 2115	6450
GAC AAC TTA GCA GTG CTG CAC ACG GCT GAG GCA GGT GGA AGG GCG TAC Asp Asn Leu Ala Val Leu His Thr Ala Glu Ala Gly Gly Arg Ala Tyr 2120 2125 2130	6498
AAC CAT GCT CTC AGT GAA CTG CCG GAG ACC CTG GAG ACA TTG CTT TTA Asn His Ala Leu Ser Glu Leu Pro Glu Thr Leu Glu Thr Leu Leu Leu 2135 2140 2145 2150	6546
CTG ACA CTT CTG GCT ACA GTC ACG GGA GGG ATC TTT TTA TTC TTG ATG Leu Thr Leu Leu Ala Thr Val Thr Gly Gly Ile Phe Leu Phe Leu Met 2155 2160 2165	6594
AGC GGA AGG GGC ATA GGG AAG ATG ACC CTG GGA ATG TGC TGC ATA ATC Ser Gly Arg Gly Ile Gly Lys Met Thr Leu Gly Met Cys Cys Ile Ile 2170 2175 2180	6642
ACG GCT AGC ATC CTC CTA TGG TAC GCA CAA ATA CAG CCA CAC TGG ATA Thr Ala Ser Ile Leu Leu Trp Tyr Ala Gln Ile Gln Pro His Trp Ile 2185 2190 2195	6690
GCA GCT TCA ATA ATA CTG GAG TTT TTT CTC ATA GTT TTG CTT ATT CCA Ala Ala Ser Ile Ile Leu Glu Phe Phe Leu Ile Val Leu Leu Ile Pro 2200 2205 2210	6738
GAA CCT GAA AAA CAG AGA ACA CCC CAA GAC AAC CAA CTG ACC TAC GTT Glu Pro Glu Lys Gln Arg Thr Pro Gln Asp Asn Gln Leu Thr Tyr Val 2215 2220 2225 2230	6786
GTC ATA GCC ATC CTC ACA GTG GTG GCC GCA ACC ATG GCA AAC GAG ATG Val Ile Ala Ile Leu Thr Val Val Ala Ala Thr Met Ala Asn Glu Met 2235 2240 2245	6834
GGT TTC CTA GAA AAA ACG AAG AAA GAT CTC GGA TTG GGA AGC ATT GCA Gly Phe Leu Glu Lys Thr Lys Lys Asp Leu Gly Leu Gly Ser Ile Ala 2250 2255 2260	6882
ACC CAG CAA CCC GAG AGC AAC ATC CTG GAC ATA GAT CTA CGT CCT GCA Thr Gln Gln Pro Glu Ser Asn Ile Leu Asp Ile Asp Leu Arg Pro Ala 2265 2270 2275	6930

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TCA GCA TGG ACG CTG TAT GCC GTG GCC ACA ACA TTT GTT ACA CCA ATG Ser Ala Trp Thr Leu Tyr Ala Val Ala Thr Thr Phe Val Thr Pro Met 2280 2285 2290	6978
TTG AGA CAT AGC ATT GAA AAT TCC TCA GTG AAT GTG TCC CTA ACA GCT Leu Arg His Ser Ile Glu Asn Ser Ser Val Asn Val Ser Leu Thr Ala 2295 2300 2305 2310	7026
ATA GCC AAC CAA GCC ACA GTG TTA ATG GGT CTC GGG AAA GGA TGG CCA Ile Ala Asn Gln Ala Thr Val Leu Met Gly Leu Gly Lys Gly Trp Pro 2315 2320 2325	7074
TTG TCA AAG ATG GAC ATC GGA GTT CCC CTT CTC GCC ATT GGA TGC TAC Leu Ser Lys Met Asp Ile Gly Val Pro Leu Leu Ala Ile Gly Cys Tyr 2330 2335 2340	7122
TCA CAA GTC AAC CCC ATA ACT CTC ACA GCA GCT CTT TTC TTA TTG GTA Ser Gln Val Asn Pro Ile Thr Leu Thr Ala Ala Leu Phe Leu Leu Val 2345 2350 2355	7170
GCA CAT TAT GCC ATC ATA GGG CCA GGA CTC CAA GCA AAA GCA ACC AGA Ala His Tyr Ala Ile Ile Gly Pro Gly Leu Gln Ala Lys Ala Thr Arg 2360 2365 2370	7218
GAA GCT CAG AAA AGA GCA GCG GCG GGC ATC ATG AAA AAC CCA ACT GTC Glu Ala Gln Lys Arg Ala Ala Ala Gly Ile Met Lys Asn Pro Thr Val 2375 2380 2385 2390	7266
GAT GGA ATA ACA GTG ATT GAC CTA GAT CCA ATA CCT TAT GAT CCA AAG Asp Gly Ile Thr Val Ile Asp Leu Asp Pro Ile Pro Tyr Asp Pro Lys 2395 2400 2405	7314
TTT GAA AAG CAG TTG GGA CAA GTA ATG CTC CTA GTC CTC TGC GTG ACT Phe Glu Lys Gln Leu Gly Gln Val Met Leu Leu Val Leu Cys Val Thr 2410 2415 2420	7362
CAA GTA TTG ATG ATG AGG ACT ACA TGG GCT CTG TGT GAG GCT TTA ACC Gln Val Leu Met Met Arg Thr Thr Trp Ala Leu Cys Glu Ala Leu Thr 2425 2430 2435	7410
TTA GCT ACC GGG CCC ATC TCC ACA TTG TGG GAA GGA AAT CCA GGG AGG Leu Ala Thr Gly Pro Ile Ser Thr Leu Trp Glu Gly Asn Pro Gly Arg 2440 2445 2450	7458
TTT TGG AAC ACT ACC ATT GCG GTG TCA ATG GCT AAC ATT TTT AGA GGG Phe Trp Asn Thr Thr Ile Ala Val Ser Met Ala Asn Ile Phe Arg Gly 2455 2460 2465 2470	7506
AGT TAC TTG GCC GGA GCT GGA CTT CTC TTT TCT ATT ATG AAG AAC ACA Ser Tyr Leu Ala Gly Ala Gly Leu Leu Phe Ser Ile Met Lys Asn Thr 2475 2480 2485	7554
ACC AAC ACA AGA AGG GGA ACT GGC AAC ATA GGA GAG ACG CTT GGA GAG Thr Asn Thr Arg Arg Gly Thr Gly Asn Ile Gly Glu Thr Leu Gly Glu 2490 2495 2500	7602
AAA TGG AAA AGC CGA TTG AAC GCA TTG GGA AAA AGT GAA TTC CAG ATC Lys Trp Lys Ser Arg Leu Asn Ala Leu Gly Lys Ser Glu Phe Gln Ile 2505 2510 2515	7650

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TAC AAG AAA AGT GGA ATC CAG GAA GTG GAT AGA ACC TTA GCA AAA GAA Tyr Lys Lys Ser Gly Ile Gln Glu Val Asp Arg Thr Leu Ala Lys Glu 2520 2525 2530	7698
GGC ATT AAA AGA GGA GAA ACG GAC CAT CAC GCT GTG TCG CGA GGC TCA Gly Ile Lys Arg Gly Glu Thr Asp His His Ala Val Ser Arg Gly Ser 2535 2540 2545 2550	7746
GCA AAA CTG AGA TGG TTC GTT GAG AGA AAC ATG GTC ACA CCA GAA GGG Ala Lys Leu Arg Trp Phe Val Glu Arg Asn Met Val Thr Pro Glu Gly 2555 2560 2565	7794
AAA GTA GTG GAC CTC GGT TGT GGC AGA GGA GGC TGG TCA TAC TAT TGT Lys Val Val Asp Leu Gly Cys Gly Arg Gly Gly Trp Ser Tyr Tyr Cys 2570 2575 2580	7842
GGA GGA CTA AAG AAT GTA AGA GAA GTC AAA GGC CTA ACA AAA GGA GGA Gly Gly Leu Lys Asn Val Arg Glu Val Lys Gly Leu Thr Lys Gly Gly 2585 2590 2595	7890
CCA GGA CAC GAA GAA CCC ATC CCC ATG TCA ACA TAT GGG TGG AAT CTA Pro Gly His Glu Glu Pro Ile Pro Met Ser Thr Tyr Gly Trp Asn Leu 2600 2605 2610	7938
GTG CGT CTT CAA AGT GGA GTT GAC GTT TTC TTC ATC CCG CCA GAA AAG Val Arg Leu Gln Ser Gly Val Asp Val Phe Phe Ile Pro Pro Glu Lys 2615 2620 2625 2630	7986
TGT GAC ACA TTA TTG TGT GAC ATA GGG GAG TCA TCA CCA AAT CCC ACA Cys Asp Thr Leu Leu Cys Asp Ile Gly Glu Ser Ser Pro Asn Pro Thr 2635 2640 2645	8034
GTG GAA GCA GGA CGA ACA CTC AGA GTC CTT AAC TTA GTA GAA AAT TGG Val Glu Ala Gly Arg Thr Leu Arg Val Leu Asn Leu Val Glu Asn Trp 2650 2655 2660	8082
TTG AAC AAC AAC ACT CAA TTT TGC ATA AAG GTT CTC AAC CCA TAT ATG Leu Asn Asn Asn Thr Gln Phe Cys Ile Lys Val Leu Asn Pro Tyr Met 2665 2670 2675	8130
CCC TCA GTC ATA GAA AAA ATG GAA GCA CTA CAA AGG AAA TAT GGA GGA Pro Ser Val Ile Glu Lys Met Glu Ala Leu Gln Arg Lys Tyr Gly Gly 2680 2685 2690	8178
GCC TTA GTG AGG AAT CCA CTC TCA CGA AAC TCC ACA CAT GAG ATG TAC Ala Leu Val Arg Asn Pro Leu Ser Arg Asn Ser Thr His Glu Met Tyr 2695 2700 2705 2710	8226
TGG GTA TCC AAT GCT TCC GGG AAC ATA GTG TCA TCA GTG AAC ATG ATT Trp Val Ser Asn Ala Ser Gly Asn Ile Val Ser Ser Val Asn Met Ile 2715 2720 2725	8274
TCA AGG ATG TTG ATC AAC AGA TTT ACA ATG AGA TAC AAG AAA GCC ACT Ser Arg Met Leu Ile Asn Arg Phe Thr Met Arg Tyr Lys Lys Ala Thr 2730 2735 2740	8322
TAC GAG CCG GAT GTT GAC CTC GGA AGC GGA ACC CGT AAC ATC GGG ATT Tyr Glu Pro Asp Val Asp Leu Gly Ser Gly Thr Arg Asn Ile Gly Ile 2745 2750 2755	8370

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GAA AGT GAG ATA CCA AAC CTA GAT ATA ATT GGG AAA AGA ATA GAA AAA Glu Ser Glu Ile Pro Asn Leu Asp Ile Ile Gly Lys Arg Ile Glu Lys 2760 2765 2770	8418
ATA AAG CAA GAG CAT GAA ACA TCA TGG CAC TAT GAC CAA GAC CAC CCA Ile Lys Gln Glu His Glu Thr Ser Trp His Tyr Asp Gln Asp His Pro 2775 2780 2785 2790	8466
TAC AAA ACG TGG GCA TAC CAT GGT AGC TAT GAA ACA AAA CAG ACT GGA Tyr Lys Thr Trp Ala Tyr His Gly Ser Tyr Glu Thr Lys Gln Thr Gly 2795 2800 2805	8514
TCA GCA TCA TCC ATG GTC AAC GGA GTG GTC AGG CTG CTG ACA AAA CCT Ser Ala Ser Ser Met Val Asn Gly Val Val Arg Leu Leu Thr Lys Pro 2810 2815 2820	8562
TGG GAC GTC GTC CCC ATG GTG ACA CAG ATG GCA ATG ACA GAC ACG ACT Trp Asp Val Val Pro Met Val Thr Gln Met Ala Met Thr Asp Thr Thr 2825 2830 2835	8610
CCA TTT GGA CAA CAG CGC GTT TTT AAA GAG AAA GTG GAC ACG AGA ACC Pro Phe Gly Gln Gln Arg Val Phe Lys Glu Lys Val Asp Thr Arg Thr 2840 2845 2850	8658
CAA GAA CCG AAA GAA GGC ACG AAG AAA CTA ATG AAA ATA ACA GCA GAG Gln Glu Pro Lys Glu Gly Thr Lys Lys Leu Met Lys Ile Thr Ala Glu 2855 2860 2865 2870	8706
TGG CTT TGG AAA GAA TTA GGG AAG AAA AAG ACA CCC AGG ATG TGC ACC Trp Leu Trp Lys Glu Leu Gly Lys Lys Lys Thr Pro Arg Met Cys Thr 2875 2880 2885	8754
AGA GAA GAA TTC ACA AGA AAG GTG AGA AGC AAT GCA GCC TTG GGG GCC Arg Glu Glu Phe Thr Arg Lys Val Arg Ser Asn Ala Ala Leu Gly Ala 2890 2895 2900	8802
ATA TTC ACT GAT GAG AAC AAG TGG AAG TCG GCA CGT GAG GCT GTT GAA Ile Phe Thr Asp Glu Asn Lys Trp Lys Ser Ala Arg Glu Ala Val Glu 2905 2910 2915	8850
GAT AGT AGG TTT TGG GAG CTG GTT GAC AAG GAA AGG AAT CTC CAT CTT Asp Ser Arg Phe Trp Glu Leu Val Asp Lys Glu Arg Asn Leu His Leu 2920 2925 2930	8898
GAA GGA AAG TGT GAA ACA TGT GTG TAC AAC ATG ATG GGA AAA AGA GAG Glu Gly Lys Cys Glu Thr Cys Val Tyr Asn Met Met Gly Lys Arg Glu 2935 2940 2945 2950	8946
AAG AAG CTA GGG GAA TTC GGC AAG GCA AAA GGC AGC AGA GCC ATA TGG Lys Lys Leu Gly Glu Phe Gly Lys Ala Lys Gly Ser Arg Ala Ile Trp 2955 2960 2965	8994
TAC ATG TGG CTT GGA GCA CGC TTC TTA GAG TTT GAA GCC CTA GGA TTC Tyr Met Trp Leu Gly Ala Arg Phe Leu Glu Phe Glu Ala Leu Gly Phe 2970 2975 2980	9042
TTA AAT GAA GAT CAC TGG TTC TCC AGA GAG AAC TCC CTG AGT GGA GTG Leu Asn Glu Asp His Trp Phe Ser Arg Glu Asn Ser Leu Ser Gly Val 2985 2990 2995	9090

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GAA GGA GAA GGG CTG CAC AAG CTA GGT TAC ATT CTA AGA GAC GTG AGC Glu Gly Glu Gly Leu His Lys Leu Gly Tyr Ile Leu Arg Asp Val Ser 3000 3005 3010	9138
AAG AAA GAG GGA GGA GCA ATG TAT GCC GAT GAC ACC GCA GGA TGG GAT Lys Lys Glu Gly Gly Ala Met Tyr Ala Asp Asp Thr Ala Gly Trp Asp 3015 3020 3025 3030	9186
ACA AGA ATC ACA CTA GAA GAC KKA AAA AAT GAA GAA ATG GTA ACA AAC Thr Arg Ile Thr Leu Glu Asp Xaa Lys Asn Glu Glu Met Val Thr Asn 3035 3040 3045	9234
CAC ATG GAA GGA GAA CAC AAG AAA CTA GCC GAG GCC ATT TTC AAA CTA His Met Glu Gly Glu His Lys Lys Leu Ala Glu Ala Ile Phe Lys Leu 3050 3055 3060	9282
ACG TAC CAA AAC AAG GTG GTG CGT GTG CAA AGA CCA ACA CCA AGA GGC Thr Tyr Gln Asn Lys Val Val Arg Val Gln Arg Pro Thr Pro Arg Gly 3065 3070 3075	9330
ACA GTA ATG GAC ATC ATA TCG AGA AGA GAC CAA AGA GGT AGT GGA CAA Thr Val Met Asp Ile Ile Ser Arg Arg Asp Gln Arg Gly Ser Gly Gln 3080 3085 3090	9378
GTT GGC ACC TAT GGA CTC AAT ACT TTC ACC AAT ATG GAA GCC CAA CTA Val Gly Thr Tyr Gly Leu Asn Thr Phe Thr Asn Met Glu Ala Gln Leu 3095 3100 3105 3110	9426
ATC AGA CAG ATG GAG GGA GAA GGA GTC TTT AAA AGC ATT CAG CAC CTA Ile Arg Gln Met Glu Gly Glu Gly Val Phe Lys Ser Ile Gln His Leu 3115 3120 3125	9474
ACA ATC ACA GAA GAA ATC GCT GTG CAA AAC TGG TTA GCA AGA GTG GGG Thr Ile Thr Glu Ile Ala Val Gln Asn Trp Leu Ala Arg Val Gly 3130 3135 3140	9522
CGC GAA AGG TTA TCA AGA ATG GCC ATC AGT GGA GAT GAT TGT GTT GTG Arg Glu Arg Leu Ser Arg Met Ala Ile Ser Gly Asp Asp Cys Val Val 3145 3150 3155	9570
AAA CCT TTA GAT GAC AGG TTC GCA AGC GCT TTA ACA GCT CTA AAT GAC Lys Pro Leu Asp Asp Arg Phe Ala Ser Ala Leu Thr Ala Leu Asn Asp 3160 3165 3170	9618
ATG GGA AAG ATT AGG AAA GAC ATA CAA CAA TGG GAA CCT TCA AGA GGA Met Gly Lys Ile Arg Lys Asp Ile Gln Gln Trp Glu Pro Ser Arg Gly 3175 3180 3185 3190	9666
TGG AAT GAT TGG ACA CAA GTG CCC TTC TGT TCA CAC CAT TTC CAT GAG Trp Asn Asp Trp Thr Gln Val Pro Phe Cys Ser His His Phe His Glu 3195 3200 3205	9714
TTA ATC ATG AAA GAC GGT CGC GTA CTC GTT GTT CCA TGT AGA AAC CAA Leu Ile Met Lys Asp Gly Arg Val Leu Val Val Pro Cys Arg Asn Gln 3210 3215 3220	9762
GAT GAA CTG ATT GGC AGA GCC CGA ATC TCC CAA GGA GCA GGG TGG TCT Asp Glu Leu Ile Gly Arg Ala Arg Ile Ser Gln Gly Ala Gly Trp Ser 3225 3230 3235	9810

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TTG CGG GAG ACG GCC TGT TTG GGG AAG TCT TAC GCC CAA ATG TGG AGC Leu Arg Glu Thr Ala Cys Leu Gly Lys Ser Tyr Ala Gln Met Trp Ser 3240 3245 3250	9858
TTG ATG TAC TTC CAC AGA CGC GAC CTC AGG CTG GCG GCA AAT GCT ATT Leu Met Tyr Phe His Arg Arg Asp Leu Arg Leu Ala Ala Asn Ala Ile 3255 3260 3265 3270	9906
TGC TCG GCA GTA CCA TCA CAT TGG GTT CCA ACA AGT CGA ACA ACC TGG Cys Ser Ala Val Pro Ser His Trp Val Pro Thr Ser Arg Thr Thr Trp 3275 3280 3285	9954
TCC ATA CAT GCT AAA CAT GAA TGG ATG ACA ACG GAA GAC ATG CTG ACA Ser Ile His Ala Lys His Glu Trp Met Thr Thr Glu Asp Met Leu Thr 3290 3295 3300	10002
GTC TGG AAC AGG GTG TGG ATT CAA GAA AAC CCA TGG ATG GAA GAC AAA Val Trp Asn Arg Val Trp Ile Gln Glu Asn Pro Trp Met Glu Asp Lys 3305 3310 3315	10050
ACT CCA GTG GAA TCA TGG GAG GAA ATC CCA TAC TTG GGG AAA AGA GAA Thr Pro Val Glu Ser Trp Glu Glu Ile Pro Tyr Leu Gly Lys Arg Glu 3320 3325 3330	10098
GAC CAA TGG TGC GGC TCA TTG ATT GGG TTA ACA AGC AGG GCC ACC TGG Asp Gln Trp Cys Gly Ser Leu Ile Gly Leu Thr Ser Arg Ala Thr Trp 3335 3340 3345 3350	10146
GCA AAG AAC ATC CAA GCA GCA ATA AAT CAA GTT AGA TCC CTT ATA GGC Ala Lys Asn Ile Gln Ala Ala Ile Asn Gln Val Arg Ser Leu Ile Gly 3355 3360 3365	10194
AAT GAA GAA TAC ACA GAT TAC ATG CCA TCC ATG AAA AGA TTC AGA AGA Asn Glu Glu Tyr Thr Asp Tyr Met Pro Ser Met Lys Arg Phe Arg Arg 3370 3375 3380	10242
GAA GAG GAA GAA GCA GGA GTT CTG TGG TAGAAAGCAA AACTAACATG AAACAAGG Glu Glu Glu Glu Ala Gly Val Leu Trp 3385 3390	10297
CTAGAAGTCA GGTCGGATTA AGCCATAGTA CGGAAAAAAC TATGCTACCT GTGAGCCCCG	10357
TCCAAGGACG TTAAAAGAAG TCAGGCCATC ATAAATGCCA TAGCTTGAGT AAACATATGCA	10417
GCCTGTAGCT CCACCTGAGA AGGTGTAAAA AATCCGGGAG GCCACAAACC ATGGAAGCTG	10477
TACGCATGGC GTAGTGGACT AGCGGTTAGA GAGGACCCCT CCCTTACAAA TCGCAGCAAC	10537
AATGGGGGCC CAAGGCGAGA TGAAGCTGTA GTCTCGCTGG AAGGACTAGA GGTTAGAGGA	10597
GACCCCCCG AAACAAAAAA CAGCATATTG ACGCTGGGAA AGACCAGAGA TCCTGCTGTC	10657
TCCTCAGCAT CATTCCAGGC ACAGAACGCC AGAAAATGGA ATGGTGCTGT TGAATCAACA	10717
GGTTCT	10723

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10723 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

1.22

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 97...10269
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGTTGTTAGT CTACGTGGAC CGACAAAGAC AGATTCTTTG AGGGAGCTAA GCTCAATGTA	60
GTTCTAACAG TTTTSTAATT AGAGAGCAGA TCTCTG ATG AAT AAC CAA CGG AAA	114
Met Asn Asn Gln Arg Lys	
1 5	
AAG GCG AAA AAC ACG CCT TTC AAT ATG CTG AAA CGC GAG AGA AAC CGC	162
Lys Ala Lys Asn Thr Pro Phe Asn Met Leu Lys Arg Glu Arg Asn Arg	
10 15 20	
GTG TCG ACT GTG CAA CAG CTG ACA AAG AGA TTC TCA CTT GGA ATG CTG	210
Val Ser Thr Val Gln Gln Leu Thr Lys Arg Phe Ser Leu Gly Met Leu	
25 30 35	
CAG GGA CGA GGA CCA TTA AAA CTG TTC ATG GCC CTG GTG GCG TTC CTT	258
Gln Gly Arg Gly Pro Leu Lys Leu Phe Met Ala Leu Val Ala Phe Leu	
40 45 50	
CGT TTC CTA ACA ATC CCA CCA ACA GCA GGG ATA TTG AAG AGA TGG GGA	306
Arg Phe Leu Thr Ile Pro Pro Thr Ala Gly Ile Leu Lys Arg Trp Gly	
55 60 65 70	
ACA ATT AAA AAA TCA AAA GCT ATT AAT GTT TTG AGA GGG TTC AGG AAA	354
Thr Ile Lys Lys Ser Lys Ala Ile Asn Val Leu Arg Gly Phe Arg Lys	
75 80 85	
GAG ATT GGA AGG ATG CTG AAC ATC TTG AAT AGG AGA CGC AGA TCT GCA	402
Glu Ile Gly Arg Met Leu Asn Ile Leu Asn Arg Arg Arg Arg Ser Ala	
90 95 100	
GGC ATG ATC ATT ATG CTG ATT CCA ACA GTG ATG GCG TTC CAT TTA ACC	450
Gly Met Ile Ile Met Leu Ile Pro Thr Val Met Ala Phe His Leu Thr	
105 110 115	
ACA CGT AAC GGA GAA CCA CAC ATG ATC GTC AGC AGA CAA GAG AAA GGG	498
Thr Arg Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly	
120 125 130	
AAA AGT CTT CTG TTT AAA ACA GAG GTT GGC GTG AAC ATG TGT ACC CTC	546
Lys Ser Leu Leu Phe Lys Thr Glu Val Gly Val Asn Met Cys Thr Leu	
135 140 145 150	
ATG GCC ATG GAC CTT GGT GAA TTG TGT GAA GAC ACA ATC ACG TAC AAG	594
Met Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys	
155 160 165	
TGT CCC CTT CTC AGG CAG AAT GAG CCA GAA GAC ATA GAC TGT TGG TGC	642
Cys Pro Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys	
170 175 180	
NAC TCT ACG TCC ACG TGG GTA ACT TAT GGG ACG TGT ACC ACC ATG GGA	690
Xaa Ser Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly	
185 190 195	

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GAA Glu 200	CAT His	AGA Arg	AGA Arg	GAA Glu	AAA Lys	AGA Arg 205	TCA Ser	GTG Val	GCA Ala	CTC Leu	GTT Val 210	CCA Pro	CAT His	GTG Val	GGA Gly	738
ATG Met 215	GGA Gly	CTG Leu	GAG Glu	ACA Thr	CGA Arg 220	ACT Thr	GAA Glu	ACA Thr	TGG Trp	ATG Met 225	TCA Ser	TCA Ser	GAA Glu	GGG Gly	GCC Ala 230	786
TGG Trp	AAA Lys	CAT His	GTC Val	CAG Gln 235	AGA Arg	ATT Ile	GAA Glu	ACT Thr	TGG Trp 240	ATC Ile	TTG Leu	AGA Arg	CAT His	CCA Pro 245	GGC Gly	834
TTC Phe	ACC Thr	ATG Met	ATG Met 250	GCA Ala	GCA Ala	ATC Ile	CTG Leu	GCA Ala 255	TAC Tyr	ACC Thr	ATA Ile	GGA Gly	ACG Thr 260	ACA Thr	CAT His	882
TTC Phe	CAA Gln	AGA Arg 265	GCC Ala	CTG Leu	ATT Ile	TTC Phe 270	ATC Ile	TTA Leu	CTG Leu	ACA Thr	GCT Ala	GTC Val 275	ACT Thr	CCT Pro	TCA Ser	930
ATG Met 280	ACA Thr	ATG Met	CGT Arg	TGC Cys	ATA Ile	GGA Gly 285	ATG Met	TCA Ser	AAT Asn	AGA Arg	GAC Asp 290	TTT Phe	GTG Val	GAA Glu	GGG Gly	978
GTT Val 295	TCA Ser	GGA Gly	GGA Gly	AGC Ser	TGG Trp 300	GTT Val	GAC Asp	ATA Ile	GTC Val	TTA Leu 305	GAA Glu	CAT His	GGA Gly	AGC Ser	TGT Cys 310	1026
GTG Val	ACG Thr	ACG Thr	ATG Met	GCA Ala 315	AAA Lys	AAC Asn	AAA Lys	CCA Pro	ACA Thr 320	TTG Leu	GAT Asp	TTT Phe	GAA Glu	CTG Leu 325	ATA Ile	1074
AAA Lys	ACA Thr	GAA Glu	GCC Ala 330	AAA Lys	CAG Gln	CCT Pro	GCC Ala	ACC Thr 335	CTA Leu	AGG Arg	AAG Lys	TAC Tyr	TGT Cys 340	ATA Ile	GAG Glu	1122
GCA Ala	AAG Lys	CTA Leu 345	ACC Thr	NAC Xaa	ACA Thr	ACA Thr	ACA Thr 350	GAA Glu	TCT Ser	CGC Arg	TGC Cys	CCA Pro 355	ACA Thr	CAA Gln	GGG Gly	1170
GAA Glu 360	CCC Pro	AGC Ser	CTA Leu	AAT Asn	GAA Glu	GAG Glu 365	CAG Gln	GAC Asp	AAA Lys	AGG Arg	TTC Phe 370	GTC Val	TGC Cys	AAA Lys	CAC His	1218
TCC Ser 375	ATG Met	GTA Val	GAC Asp	AGA Arg	GGA Gly 380	TGG Trp	GGA Gly	AAT Asn	GGA Gly 385	TGT Cys	GGA Gly	CTA Leu	TTT Phe	GGA Gly	AAG Lys 390	1266
GGA Gly	GGC Gly	ATT Ile	GTG Val	ACC Thr 395	TGT Cys	GCT Ala	ATG Met	TTC Phe	AGA Arg 400	TGC Cys	AAA Lys	AAG Lys	AAC Asn	ATG Met 405	GAA Glu	1314
GGA Gly	AAA Lys	GTT Val	GTG Val 410	CAA Gln	CCA Pro	GAA Glu	AAC Asn	TTG Leu 415	GAA Glu	TAC Tyr	ACC Thr	ATT Ile	GTG Val 420	ATA Ile	ACA Thr	1362
CCT Pro	CAC His	TCA Ser 425	GGG Gly	GAA Glu	GAG Glu	CAT His	GCA Ala 430	GTC Val	GGA Gly	NAT Xaa	GAC Asp	ACA Thr	GGA Gly	AAA Lys	CAT His	1410

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GGC Gly	AAG Lys	GAA Glu	ATC Ile	AAA Lys	ATA Ile	ACA Thr	CCA Pro	CAG Gln	AGT Ser	TCC Ser	ATC Ile	ACA Thr	GAA Glu	GCA Ala	GAA Glu	1458
440						445					450					
TTG Leu	ACA Thr	GGT Gly	TAT Tyr	GGC Gly	ACT Thr	GTC Val	ACA Thr	ATG Met	GAG Glu	TGC Cys	TCT Ser	CCA Pro	AGA Arg	ACG Thr	GGC Gly	1506
455					460					465					470	
CTC Leu	GAC Asp	TTC Phe	AAT Asn	GAG Glu	ATG Met	GTG Val	TTG Leu	CTG Leu	CAG Gln	ATG Met	GAA Glu	AAT Asn	AAA Lys	GCT Ala	TGG Trp	1554
				475					480					485		
CTG Leu	GTG Val	CAC His	AGG Arg	CAA Gln	TGG Trp	TTC Phe	CTA Leu	GAC Asp	CTG Leu	CCG Pro	TTA Leu	CCA Pro	TGG Trp	TTG Leu	CCC Pro	1602
			490					495					500			
GGA Gly	GCG Ala	GAC Asp	ACA Thr	CAA Gln	GGG Gly	TCA Ser	AAT Asn	TGG Trp	ATA Ile	CAG Gln	AAA Lys	GAG Glu	ACA Thr	TTG Leu	GTC Val	1650
		505					510					515				
ACT Thr	TTC Phe	AAA Lys	AAT Asn	CCC Pro	CAT His	GCG Ala	AAG Lys	AAA Lys	CAG Gln	GAT Asp	GTT Val	GTT Val	GTT Val	TTA Leu	GGA Gly	1698
520						525					530					
TCC Ser	CAA Gln	GAA Glu	GGG Gly	GCC Ala	ATG Met	CAC His	ACA Thr	GCA Ala	CTT Leu	ACA Thr	GGG Gly	GCC Ala	ACA Thr	GAA Glu	ATC Ile	1746
535					540					545					550	
CAA Gln	ATG Met	TCA Ser	TCA Ser	GGA Gly	AAC Asn	TTA Leu	CTC Leu	TTC Phe	ACA Thr	GGA Gly	CAT His	CTC Leu	AAG Lys	TGC Cys	AGG Arg	1794
				555					560					565		
CTG Leu	AGA Arg	ATG Met	GAC Asp	AAG Lys	CTA Leu	CAG Gln	CTC Leu	AAA Lys	GGA Gly	ATG Met	TCA Ser	TAC Tyr	TCT Ser	ATG Met	TGC Cys	1842
			570					575					580			
ACA Thr	GGA Gly	AAG Lys	TTT Phe	AAA Lys	GTT Val	GTG Val	AAG Lys	GAA Glu	ATA Ile	GCA Ala	GAA Glu	ACA Thr	CAA Gln	CAT His	GGA Gly	1890
		585					590					595				
ACA Thr	ATA Ile	GTT Val	ATC Ile	AGA Arg	GTG Val	CAA Gln	TAT Tyr	GAA Glu	GGG Gly	GAC Asp	GGC Gly	TCT Ser	CCA Pro	TGC Cys	AAG Lys	1938
	600					605					610					
ATC Ile	CCT Pro	TTT Phe	GAG Glu	ATA Ile	ATG Met	GAT Asp	TTG Leu	GAA Glu	AAA Lys	AGA Arg	CAT His	GTC Val	TTA Leu	GGT Gly	CGC Arg	1986
615					620					625					630	
CTG Leu	ATT Ile	ACA Thr	GTC Val	AAC Asn	CCA Pro	ATT Ile	GTG Val	ACA Thr	GAA Glu	AAA Lys	GAT Asp	AGC Ser	CCA Pro	GTC Val	AAC Asn	2034
				635					640					645		
ATA Ile	GAA Glu	GCA Ala	GAA Glu	CCT Pro	CCA Pro	TTT Phe	GGA Gly	GAC Asp	AGC Ser	TAC Tyr	ATC Ile	ATC Ile	ATA Ile	GGA Gly	GTA Val	2082
			650					655					660			
GAG Glu	CCG Pro	GGA Gly	CAA Gln	CTG Leu	AAG Lys	CTC Leu	AAC Asn	TGG Trp	TTT Phe	AAG Lys	AAA Lys	GGA Gly	AGT Ser	TCT Ser	ATC Ile	2130
		665					670					675				

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GGC Gly	CAA Gln	ATG Met	TTT Phe	GAG Glu	ACA Thr	ACA Thr	ATG Met	AGG Arg	GGG Gly	GCG Ala	AAG Lys	AGA Arg	ATG Met	GCC Ala	ATT Ile	2178
680						685					690					
TTA Leu	GGT Gly	GAC Asp	ACA Thr	GCC Ala	TGG Trp	GAT Asp	TTT Phe	GGA Gly	TCC Ser	TTG Leu	GGA Gly	GGA Gly	GTG Val	TTT Phe	ACA Thr	2226
695					700					705					710	
TCT Ser	ATA Ile	GGA Gly	AAG Lys	GCT Ala	CTC Leu	CAC His	CAA Gln	GTC Val	TTT Phe	GGA Gly	GCA Ala	ATC Ile	TAT Tyr	GGA Gly	GCT Ala	2274
				715					720					725		
GCC Ala	TTC Phe	AGT Ser	GGG Gly	GTT Val	TCA Ser	TGG Trp	ACT Thr	ATG Met	AAA Lys	ATC Ile	CTC Leu	ATA Ile	GGA Gly	GTC Val	ATT Ile	2322
			730					735					740			
ATC Ile	ACA Thr	TGG Trp	ATA Ile	GGA Gly	ATG Met	AAT Asn	TCA Ser	CGC Arg	AGC Ser	ACC Thr	TCA Ser	CTG Leu	TCT Ser	GTG Val	ACA Thr	2370
		745					750					755				
CTA Leu	GTA Val	TTG Leu	GTG Val	GGA Gly	ATT Ile	GTG Val	ACA Thr	CTG Leu	TAT Tyr	TTG Leu	GGA Gly	GTC Val	ATG Met	GTG Val	CAG Gln	2418
	760					765					770					
GCC Ala	GAT Asp	AGT Ser	GGT Gly	TGC Cys	GTT Val	GTG Val	AGC Ser	TGG Trp	AAA Lys	AAC Asn	AAA Lys	GAA Glu	CTG Leu	AAA Lys	TGT Cys	2466
775					780					785					790	
GGC Gly	AGT Ser	GGG Gly	ATT Ile	TTC Phe	ATC Ile	ACA Thr	GAC Asp	AAC Asn	GTG Val	CAC His	ACA Thr	TGG Trp	ACA Thr	GAA Glu	CAA Gln	2514
				795					800					805		
TAC Tyr	AAG Lys	TTC Phe	CAA Gln	CCA Pro	GAA Glu	TCC Ser	CCT Pro	TCA Ser	AAA Lys	CTA Leu	GCT Ala	TCA Ser	GCT Ala	ATC Ile	CAG Gln	2562
			810					815					820			
AAA Lys	GCC Ala	CAT His	GAA Glu	GAG Glu	GAC Asp	ATT Ile	TGT Cys	GGA Gly	ATC Ile	CGC Arg	TCA Ser	GTA Val	ACA Thr	AGA Arg	CTG Leu	2610
		825					830					835				
GAG Glu	AAT Asn	CTG Leu	ATG Met	TGG Trp	AAA Lys	CAA Gln	ATA Ile	ACA Thr	CCA Pro	GAA Glu	TTG Leu	AAT Asn	CAC His	ATT Ile	CTA Leu	2658
	840					845					850					
TCA Ser	GAA Glu	AAT Asn	GAG Glu	GTG Val	AAG Lys	TTA Leu	ACT Thr	ATT Ile	ATG Met	ACA Thr	GGA Gly	GAC Asp	ATC Ile	AAA Lys	GGA Gly	2706
855					860					865					870	
ATC Ile	ATG Met	CAG Gln	GCA Ala	GGA Gly	AAA Lys	CGA Arg	TCT Ser	CTG Leu	CGG Arg	CCT Pro	CAG Gln	CCC Pro	ACT Thr	GAG Glu	CTG Leu	2754
				875					880					885		
AAG Lys	TAT Tyr	TCA Ser	TGG Trp	AAA Lys	ACA Thr	TGG Trp	GGC Gly	AAA Lys	GCA Ala	AAA Lys	ATG Met	CTC Leu	TCT Ser	ACA Thr	GAG Glu	2802
			890				895					900				
TCT Ser	CAT His	NAC Xaa	CAG Gln	ACC Thr	TTT Phe	CTC Leu	ATT Ile	GAT Asp	GGC Gly	CCC Pro	GAA Glu	ACA Thr	GCA Ala	GAA Glu	TGC Cys	2850

905

910

915

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CCC Pro	AAC Asn	ACA Thr	AAT Asn	AGA Arg	GCT Ala	TGG Trp	AAT Asn	TCG Ser	TTG Leu	GAA Glu	GTT Val	GAA Glu	GAC Asp	TAT Tyr	GGC Gly	2898
920						925					930					
TTT Phe	GGA Gly	GTA Val	TTC Phe	ACC Thr	ACC Thr	AAT Asn	ATA Ile	TGG Trp	CTA Leu	AAA Lys	TTG Leu	AAA Lys	GAA Glu	AAA Lys	CAG Gln	2946
935					940					945					950	
GAT Asp	GTA Val	TTC Phe	TGC Cys	GAC Asp	TCA Ser	AAA Lys	CTC Leu	ATG Met	TCA Ser	GCG Ala	GCC Ala	ATA Ile	AAA Lys	GAC Asp	AAC Asn	2994
				955					960					965		
AGA Arg	GCC Ala	GTC Val	CAT His	GCC Ala	GAT Asp	ATG Met	GGT Gly	TAT Tyr	TGG Trp	ATA Ile	GAA Glu	AGT Ser	GCA Ala	CTC Leu	NAT Xaa	3042
			970					975					980			
GAC Asp	ACA Thr	TGG Trp	AAG Lys	ATA Ile	GAG Glu	AAA Lys	GCC Ala	TCT Ser	TTC Phe	ATT Ile	GAA Glu	GTT Val	AAA Lys	AAC Asn	TGC Cys	3090
		985					990					995				
CAC His	TGG Trp	CCA Pro	AAA Lys	TCA Ser	CAC His	ACC Thr	CTC Leu	TGG Trp	AGC Ser	AAT Asn	GGA Gly	GTG Val	CTA Leu	GAA Glu	AGT Ser	3138
	1000					1005					1010					
GAG Glu	ATG Met	ATA Ile	ATT Ile	CCA Pro	AAG Lys	AAT Asn	CTC Leu	GCT Ala	GGA Gly	CCA Pro	GTG Val	TCT Ser	CAA Gln	CAC His	AAC Asn	3186
1015					1020				1025						1030	
TAT Tyr	AGA Arg	CCA Pro	GGC Gly	TAC Tyr	CAT His	ACA Thr	CAA Gln	ATA Ile	ACA Thr	GGA Gly	CCA Pro	TGG Trp	CAT His	CTA Leu	GGT Gly	3234
				1035				1040					1045			
AAG Lys	CTT Leu	GAG Glu	ATG Met	GAC Asp	TTT Phe	GAT Asp	TTC Phe	TGT Cys	GAT Asp	GGA Gly	ACA Thr	ACA Thr	GTG Val	GTA Val	GTG Val	3282
			1050				1055						1060			
ACT Thr	GAG Glu	GAC Asp	TGC Cys	GGA Gly	AAT Asn	AGA Arg	GGA Gly	CCC Pro	TCT Ser	TTG Leu	AGA Arg	ACA Thr	ACC Thr	ACT Thr	GCC Ala	3330
		1065					1070					1075				
TCT Ser	GGA Gly	AAA Lys	CTC Leu	ATA Ile	ACA Thr	GAA Glu	TGG Trp	TGC Cys	TGC Cys	CGA Arg	TCT Ser	TGC Cys	ACA Thr	TTA Leu	CCA Pro	3378
	1080					1085					1090					
CCG Pro	CTA Leu	AGA Arg	TAC Tyr	AGA Arg	GGT Gly	GAG Glu	GAT Asp	GGG Gly	TGC Cys	TGG Trp	TAC Tyr	GGG Gly	ATG Met	GAA Glu	ATC Ile	3426
1095					1100				1105					1110		
AGA Arg	CCA Pro	TTG Leu	AAG Lys	GAG Glu	AAA Lys	GAA Glu	GAG Glu	AAT Asn	TTG Leu	GTC Val	AAC Asn	TCC Ser	TTG Leu	GTC Val	ACA Thr	3474
				1115				1120					1125			
GCT Ala	GGA Gly	CAT His	GGG Gly	CAG Gln	GTC Val	GAC Asp	AAC Asn	TTT Phe	TCA Ser	CTA Leu	GGA Gly	GTC Val	TTG Leu	GGA Gly	ATG Met	3522
		1130					1135						1140			
GCA Ala	TTG Leu	TTC Phe	CTG Leu	GAG Glu	GAA Glu	ATG Met	CTT Leu	AGG Arg	ACC Thr	CGA Arg	GTA Val	GGA Gly	ACG Thr	AAA Lys	CAT His	3570
	1145						1150					1155				

127

GCA ATA CTA CTA GTT GCA GTT TCT TTT GTG ACA TTG ATC ACA GGG AAC	3618
Ala Ile Leu Leu Val Ala Val Ser Phe Val Thr Leu Ile Thr Gly Asn	
1160 1165 1170	
ATG TCC TTT AGA GAC CTG GGA AGA GTG ATG GTT ATG GTA GGC GCC ACT	3666
Met Ser Phe Arg Asp Leu Gly Arg Val Met Val Met Val Gly Ala Thr	
1175 1180 1185 1190	
ATG ACG GAT GAC ATA GGT ATG GGC GTG ACT TAT CTT GCC CTA CTA GCA	3714
Met Thr Asp Asp Ile Gly Met Gly Val Thr Tyr Leu Ala Leu Leu Ala	
1195 1200 1205	
GCC TTC AAA GTC AGA CCA ACT TTT GCA GCT GGA CTA CTC TTG AGA AAG	3762
Ala Phe Lys Val Arg Pro Thr Phe Ala Ala Gly Leu Leu Arg Lys	
1210 1215 1220	
CTG ACC TCC AAG GAA TTG ATG ATG ACT ACT ATA GGA ATT GTA CTC CTC	3810
Leu Thr Ser Lys Glu Leu Met Met Thr Thr Ile Gly Ile Val Leu Leu	
1225 1230 1235	
TCC CAG AGC ACC ATA CCA GAG ACC ATT CTT GAG TTG ACT GAT GCG TTA	3858
Ser Gln Ser Thr Ile Pro Glu Thr Ile Leu Glu Leu Thr Asp Ala Leu	
1240 1245 1250	
GCC TTA GGC ATG ATG GTC CTC AAA ATG GTG AGA AAT ATG GAA AAG TAT	3906
Ala Leu Gly Met Met Val Leu Lys Met Val Arg Asn Met Glu Lys Tyr	
1255 1260 1265 1270	
CAA TTG GCA GTG ACT ATC ATG GCT ATC TTG TGC GTC CCA AAC GCA GTG	3954
Gln Leu Ala Val Thr Ile Met Ala Ile Leu Cys Val Pro Asn Ala Val	
1275 1280 1285	
ATA TTA CAA AAC GCA TGG AAA GTG AGT TGC ACA ATA TTG GCA GTG GTG	4002
Ile Leu Gln Asn Ala Trp Lys Val Ser Cys Thr Ile Leu Ala Val Val	
1290 1295 1300	
TCC GTT TCC CCA CTG TTC TTA ACA TCC TCA CAG CAA AAA ACA GAT TGG	4050
Ser Val Ser Pro Leu Phe Leu Thr Ser Ser Gln Gln Lys Thr Asp Trp	
1305 1310 1315	
ATA CCA TTA GCA TTG ACG ATC AAA GGT CTC AAT CCA ACA GCT ATT TTT	4098
Ile Pro Leu Ala Leu Thr Ile Lys Gly Leu Asn Pro Thr Ala Ile Phe	
1320 1325 1330	
CTA ACA ACC CTC TCA AGA ACC AGC AAG AAA AGG AGC TGG CCA TTA AAT	4146
Leu Thr Thr Leu Ser Arg Thr Ser Lys Lys Arg Ser Trp Pro Leu Asn	
1335 1340 1345 1350	
GAG GCT ATC ATG GCA GTC GGG ATG GTG AGC ATT TTA GCC AGT TCT CTC	4194
Glu Ala Ile Met Ala Val Gly Met Val Ser Ile Leu Ala Ser Ser Leu	
1355 1360 1365	
CTA AAA AAT GAT ATT CCC ATG ACA GGA CCA TTA GTG GCT GGA GGG CTC	4242
Leu Lys Asn Asp Ile Pro Met Thr Gly Pro Leu Val Ala Gly Gly Leu	
1370 1375 1380	
CTC ACT GTG TGC TAC GTG CTC ACT GGA CGA TCG GCC GAT TTG GAA CTG	4290
Leu Thr Val Cys Tyr Val Leu Thr Gly Arg Ser Ala Asp Leu Glu Leu	
1385 1390 1395	

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GAG AGA GCA GCC GAT GTC AAA TGG GAA GAC CAG GCA GAG ATA TCA GGA Glu Arg Ala Ala Asp Val Lys Trp Glu Asp Gln Ala Glu Ile Ser Gly 1400 1405 1410	4338
AGC AGT CCA ATC CTG TCA ATA ACA ATA TCA GAA GAT GGT AGC ATG TCG Ser Ser Pro Ile Leu Ser Ile Thr Ile Ser Glu Asp Gly Ser Met Ser 1415 1420 1425 1430	4386
ATA AAA AAT GAA GAG GAA GAA CAA ACA CTG ACC ATA CTC ATT AGA ACA Ile Lys Asn Glu Glu Glu Glu Gln Thr Leu Thr Ile Leu Ile Arg Thr 1435 1440 1445	4434
GGA TTG CTG GTG ATC TCA GGA CTT TTT CCT GTA TCA ATA CCA ATC ACG Gly Leu Leu Val Ile Ser Gly Leu Phe Pro Val Ser Ile Pro Ile Thr 1450 1455 1460	4482
GCA GCA GCA TGG TAC CTG TGG GAA GTG AAG AAA CAA CGG GCC GGA GTA Ala Ala Ala Trp Tyr Leu Trp Glu Val Lys Lys Gln Arg Ala Gly Val 1465 1470 1475	4530
TTG TGG GAT GTT CCT TCA CCC CCA CCC ATG GGA AAG GCT GAA CTG GAA Leu Trp Asp Val Pro Ser Pro Pro Met Gly Lys Ala Glu Leu Glu 1480 1485 1490	4578
GAT GGA GCC TAT AGA ATT AAG CAA AAA GGG ATT CTT GGA TAT TCC CAG Asp Gly Ala Tyr Arg Ile Lys Gln Lys Gly Ile Leu Gly Tyr Ser Gln 1495 1500 1505 1510	4626
ATC GGA GCC GGA GTT TAC AAA GAA GGA ACA TTC CAT ACA ATG TGG CAT Ile Gly Ala Gly Val Tyr Lys Glu Gly Thr Phe His Thr Met Trp His 1515 1520 1525	4674
GTC ACA CGT GGC GCT GTT CTA ATG CAT AAA GGA AAG AGG ATT GAA CCA Val Thr Arg Gly Ala Val Leu Met His Lys Gly Lys Arg Ile Glu Pro 1530 1535 1540	4722
TCA TGG GCG GAC GTC AAG AAA GAC CTA ATA TCA TAT GGA GGA GGC TGG Ser Trp Ala Asp Val Lys Lys Asp Leu Ile Ser Tyr Gly Gly Gly Trp 1545 1550 1555	4770
AAG TTA GAA GGA GAA TGG AAG GAA GGA GAA GAA GTC CAG GTA TTG GCA Lys Leu Glu Gly Glu Trp Lys Glu Gly Glu Glu Val Gln Val Leu Ala 1560 1565 1570	4818
CTG GAG CCT GGA AAA AAT CCA AGA GCC GTC CAA ACG AAA CCT GGT CTT Leu Glu Pro Gly Lys Asn Pro Arg Ala Val Gln Thr Lys Pro Gly Leu 1575 1580 1585 1590	4866
TTC AAA ACC AAC GCC GGA ACA ATA GGT GCT GTA TCT CTG GAC TTT TCT Phe Lys Thr Asn Ala Gly Thr Ile Gly Ala Val Ser Leu Asp Phe Ser 1595 1600 1605	4914
CCT GGA ACG TCA GGA TCT CCA ATT ATC GAC AAA AAA GGA AAA GTT GTG Pro Gly Thr Ser Gly Ser Pro Ile Ile Asp Lys Lys Gly Lys Val Val 1610 1615 1620	4962
GGT CTT TAT GGT AAT GGT GTT GTT ACA AGG AGT GGA GCA TAT GTG AGT Gly Leu Tyr Gly Asn Gly Val Val Thr Arg Ser Gly Ala Tyr Val Ser 1625 1630 1635	5010

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GCT ATA GCC CAG ACT GAA AAA AGC ATT GAA GAC AAC CCA GAG ATC GAA Ala Ile Ala Gln Thr Glu Lys Ser Ile Glu Asp Asn Pro Glu Ile Glu 1640 1645 1650	5058
GAT GAC ATT TTC CGA AAG AGA AGA CTG ACC ATC ATG GAC CTC CAC CCA Asp Asp Ile Phe Arg Lys Arg Arg Leu Thr Ile Met Asp Leu His Pro 1655 1660 1665 1670	5106
GGA GCG GGA AAG ACG AAG AGA TAC CTT CCG GCC ATA GTC AGA GAA GCT Gly Ala Gly Lys Thr Lys Arg Tyr Leu Pro Ala Ile Val Arg Glu Ala 1675 1680 1685	5154
ATA AAA CGG GGT TTG AGA ACA TTA ATC TTG GCC CCC ACT AGA GTT GTG Ile Lys Arg Gly Leu Arg Thr Leu Ile Leu Ala Pro Thr Arg Val Val 1690 1695 1700	5202
GCA GCT GAA ATG GAG GAA GCC CTT AGA GGA CTT CCA ATA AGA TAC CAG Ala Ala Glu Met Glu Glu Ala Leu Arg Gly Leu Pro Ile Arg Tyr Gln 1705 1710 1715	5250
ACC CCA GCC ATC AGA GCT GAG CAC ACC GGG CGG GAG ATT GTG GAC CTA Thr Pro Ala Ile Arg Ala Glu His Thr Gly Arg Glu Ile Val Asp Leu 1720 1725 1730	5298
ATG TGT CAT GCC ACA TTT ACC ATG AGG CTG CTA TCA CCA GTT AGA GTG Met Cys His Ala Thr Phe Thr Met Arg Leu Leu Ser Pro Val Arg Val 1735 1740 1745 1750	5346
CCA AAC TAC AAC CTG ATT ATC ATG GAC GAA GCC CAT TTC ACA GAC CCA Pro Asn Tyr Asn Leu Ile Ile Met Asp Glu Ala His Phe Thr Asp Pro 1755 1760 1765	5394
GCA AGT ATA GCA GCT AGA GGA TAC ATC TCA ACT CGA GTG GAG ATG GGT Ala Ser Ile Ala Ala Arg Gly Tyr Ile Ser Thr Arg Val Glu Met Gly 1770 1775 1780	5442
GAG GCA GCT GGG ATT TTT ATG ACA GCC ACT CCC CCG GGA AGC AGA GAC Glu Ala Ala Gly Ile Phe Met Thr Ala Thr Pro Pro Gly Ser Arg Asp 1785 1790 1795	5490
CCA TTT CCT CAG AGC AAT GCA CCA ATC ATA GAT GAA GAA AGA GAA ATC Pro Phe Pro Gln Ser Asn Ala Pro Ile Ile Asp Glu Glu Arg Glu Ile 1800 1805 1810	5538
CCT GAA CGT TCG TGG AAT TCC GGA CAT GAA TGG GTC ACG GAT TTT AAA Pro Glu Arg Ser Trp Asn Ser Gly His Glu Trp Val Thr Asp Phe Lys 1815 1820 1825 1830	5586
GGG AAG ACT GTT TGG TTC GTT CCA AGT ATA AAA GCA GGA AAT GAT ATA Gly Lys Thr Val Trp Phe Val Pro Ser Ile Lys Ala Gly Asn Asp Ile 1835 1840 1845	5634
GCA GCT TGC CTG AGG AAA AAT GGA AAG AAA GTG ATA CAA CTC AGT AGG Ala Ala Cys Leu Arg Lys Asn Gly Lys Lys Val Ile Gln Leu Ser Arg 1850 1855 1860	5682
AAG ACC TTT GAT TCT GAG TAT GTC AAG ACT AGA ACC AAT GAT TGG GAC Lys Thr Phe Asp Ser Glu Tyr Val Lys Thr Arg Thr Asn Asp Trp Asp 1865 1870 1875	5730

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TTC GTG GTT ACA ACT GAC ATT TCA GAA ATG GGT GCC AAT TTC AAG GCT Phe Val Val Thr Thr Asp Ile Ser Glu Met Gly Ala Asn Phe Lys Ala 1880 1885 1890	5778
GAG AGG GTT ATA GAC CCC AGA CGC TGC ATG AAA CCA GTC ATA CTA ACA Glu Arg Val Ile Asp Pro Arg Arg Cys Met Lys Pro Val Ile Leu Thr 1895 1900 1905 1910	5826
GAT GGT GAA GAG CGG GTG ATT CTG GCA GGA CCT ATG CCA GTG ACC CAC Asp Gly Glu Glu Arg Val Ile Leu Ala Gly Pro Met Pro Val Thr His 1915 1920 1925	5874
TCT AGT GCA GCA CAA AGA AGA GGG AGA ATA GGA AGA AAT CCA AAA AAT Ser Ser Ala Ala Gln Arg Arg Gly Arg Ile Gly Arg Asn Pro Lys Asn 1930 1935 1940	5922
GAG AAT GAC CAG TAC ATA TAC ATG GGG GAA CCT CTG GAA AAT GAT GAA Glu Asn Asp Gln Tyr Ile Tyr Met Gly Glu Pro Leu Glu Asn Asp Glu 1945 1950 1955	5970
GAC TGT GCA CAC TGG AAA GAA GCT AAA ATG CTC CTA GAT AAC ATC AAC Asp Cys Ala His Trp Lys Glu Ala Lys Met Leu Leu Asp Asn Ile Asn 1960 1965 1970	6018
ACG CCA GAA GGA ATC ATT CCT AGC ATG TTC GAA CCA GAG CGT GAA AAG Thr Pro Glu Gly Ile Ile Pro Ser Met Phe Glu Pro Glu Arg Glu Lys 1975 1980 1985 1990	6066
GTG GAT GCC ATT GAT GGC GAA TAC CGC TTG AGA GGA GAA GCA AGG AAA Val Asp Ala Ile Asp Gly Glu Tyr Arg Leu Arg Gly Glu Ala Arg Lys 1995 2000 2005	6114
ACC TTT GTA GAC TTA ATG AGA AGA GGA GAC CTA CCA GTC TGG TTG GCC Thr Phe Val Asp Leu Met Arg Arg Gly Asp Leu Pro Val Trp Leu Ala 2010 2015 2020	6162
TAC AGA GTG GCA GCT GAA GGC ATC AAC TAC GCA GAC AGA AGG TGG TGT Tyr Arg Val Ala Ala Glu Gly Ile Asn Tyr Ala Asp Arg Arg Trp Cys 2025 2030 2035	6210
TTT GAT GGA GTC AAG AAC AAC CAA ATC CTA GAA GAA AAC GTG GAA GTT Phe Asp Gly Val Lys Asn Asn Gln Ile Leu Glu Glu Asn Val Glu Val 2040 2045 2050	6258
GAA ATC TGG ACA AAA GAA GGG GAA AGG AAG AAA TTG AAA CCC AGA TGG Glu Ile Trp Thr Lys Glu Gly Glu Arg Lys Lys Leu Lys Pro Arg Trp 2055 2060 2065 2070	6306
TTG GAT GCT AGG ATC TAT TCT GAC CCA CTG GCG CTA AAA GAA TTT AAG Leu Asp Ala Arg Ile Tyr Ser Asp Pro Leu Ala Leu Lys Glu Phe Lys 2075 2080 2085	6354
GAA TTT GCA GCC GGA AGA AAG TCT CTG ACC CTG AAC CTA ATC ACA GAA Glu Phe Ala Ala Gly Arg Lys Ser Leu Thr Leu Asn Leu Ile Thr Glu 2090 2095 2100	6402
ATG GGT AGG CTC CCA ACC TTC ATG ACT CAG AAG GCA AGA GAC GCA CTG Met Gly Arg Leu Pro Thr Phe Met Thr Gln Lys Ala Arg Asp Ala Leu 2105 2110 2115	6450

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GAC AAC TTA GCA GTG CTG CAC ACG GCT GAG GCA GGT GGA AGG GCG TAC Asp Asn Leu Ala Val Leu His Thr Ala Glu Ala Gly Gly Arg Ala Tyr 2120 2125 2130	6498
AAC CAT GCT CTC AGT GAA CTG CCG GAG ACC CTG GAG ACA TTG CTT TTA Asn His Ala Leu Ser Glu Leu Pro Glu Thr Leu Glu Thr Leu Leu Leu 2135 2140 2145 2150	6546
CTG ACA CTT CTG GCT ACA GTC ACG GGA GGG ATC TTT TTA TTC TTG ATG Leu Thr Leu Leu Ala Thr Val Thr Gly Gly Ile Phe Leu Phe Leu Met 2155 2160 2165	6594
AGC GCA AGG GGC ATA GGG AAG ATG ACC CTG GGA ATG TGC TGC ATA ATC Ser Ala Arg Gly Ile Gly Lys Met Thr Leu Gly Met Cys Cys Ile Ile 2170 2175 2180	6642
ACG GCT AGC ATC CTC CTA TGG TAC GCA CAA ATA CAG CCA CAC TGG ATA Thr Ala Ser Ile Leu Leu Trp Tyr Ala Gln Ile Gln Pro His Trp Ile 2185 2190 2195	6690
GCA GCT TCA ATA ATA CTG GAG TTT TTT CTC ATA GTT TTG CTT ATT CCA Ala Ala Ser Ile Ile Leu Glu Phe Phe Leu Ile Val Leu Leu Ile Pro 2200 2205 2210	6738
GAA CCT GAA AAA CAG AGA ACA CCC CAA GAC AAC CAA CTG ACC TAC GTT Glu Pro Glu Lys Gln Arg Thr Pro Gln Asp Asn Gln Leu Thr Tyr Val 2215 2220 2225 2230	6786
GTC ATA GCC ATC CTC ACA GTG GTG GCC GCA ACC ATG GCA AAC GAG ATG Val Ile Ala Ile Leu Thr Val Val Ala Ala Thr Met Ala Asn Glu Met 2235 2240 2245	6834
GGT TTC CTA GAA AAA ACG AAG AAA GAT CTC GGA TTG GGA AGC ATT GCA Gly Phe Leu Glu Lys Thr Lys Lys Asp Leu Gly Leu Gly Ser Ile Ala 2250 2255 2260	6882
ACC CAG CAA CCC GAG AGC AAC ATC CTG GAC ATA GAT CTA CGT CCT GCA Thr Gln Gln Pro Glu Ser Asn Ile Leu Asp Ile Asp Leu Arg Pro Ala 2265 2270 2275	6930
TCA GCA TGG ACG CTG TAT GCC GTG GCC ACA ACA TTT GTT ACA CCA ATG Ser Ala Trp Thr Leu Tyr Ala Val Ala Thr Thr Phe Val Thr Pro Met 2280 2285 2290	6978
TTG AGA CAT AGC ATT GAA AAT TCC TCA GTG AAT GTG TCC CTA ACA GCT Leu Arg His Ser Ile Glu Asn Ser Ser Val Asn Val Ser Leu Thr Ala 2295 2300 2305 2310	7026
ATA GCC AAC CAA GCC ACA GTG TTA ATG GGT CTC GGG AAA GGA TGG CCA Ile Ala Asn Gln Ala Thr Val Leu Met Gly Leu Gly Lys Gly Trp Pro 2315 2320 2325	7074
TTG TCA AAG ATG GAC ATC GGA GTT CCC CTT CTC GCC ATT GGA TGC TAC Leu Ser Lys Met Asp Ile Gly Val Pro Leu Leu Ala Ile Gly Cys Tyr 2330 2335 2340	7122
TCA CAA GTC AAC CCC ATA ACT CTC ACA GCA GCT CTT TTC TTA TTG GTA Ser Gln Val Asn Pro Ile Thr Leu Thr Ala Ala Leu Phe Leu Leu Val 2345 2350 2355	7170

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GCA CAT TAT GCC ATC ATA GGG CCA GGA CTC CAA GCA AAA GCA ACC AGA Ala His Tyr Ala Ile Ile Gly Pro Gly Leu Gln Ala Lys Ala Thr Arg 2360 2365 2370	7218
GAA GCT CAG AAA AGA GCA GCG GCG GGC ATC ATG AAA AAC CCA ACT GTC Glu Ala Gln Lys Arg Ala Ala Ala Gly Ile Met Lys Asn Pro Thr Val 2375 2380 2385 2390	7266
GAT GGA ATA ACA GTG ATT GAC CTA GAT CCA ATA CCT TAT GAT CCA AAG Asp Gly Ile Thr Val Ile Asp Leu Asp Pro Ile Pro Tyr Asp Pro Lys 2395 2400 2405	7314
TTT GAA AAG CAG TTG GGA CAA GTA ATG CTC CTA GTC CTC TGC GTG ACT Phe Glu Lys Gln Leu Gly Gln Val Met Leu Leu Val Leu Cys Val Thr 2410 2415 2420	7362
CAA GTA TTG ATG ATG AGG ACT ACA TGG GCT CTG TGT GAG GCT TTA ACC Gln Val Leu Met Met Arg Thr Thr Trp Ala Leu Cys Glu Ala Leu Thr 2425 2430 2435	7410
TTA GCT ACC GGG CCC ATC TCC ACA TTG TGG GAA GGA AAT CCA GGG AGG Leu Ala Thr Gly Pro Ile Ser Thr Leu Trp Glu Gly Asn Pro Gly Arg 2440 2445 2450	7458
TTT TGG AAC ACT ACC ATT GCG GTG TCA ATG GCT AAC ATT TTT AGA GGG Phe Trp Asn Thr Thr Ile Ala Val Ser Met Ala Asn Ile Phe Arg Gly 2455 2460 2465 2470	7506
AGT TAC TTG GCC GGA GCT GGA CTT CTC TTT TCT ATT ATG AAG AAC ACA Ser Tyr Leu Ala Gly Ala Gly Leu Leu Phe Ser Ile Met Lys Asn Thr 2475 2480 2485	7554
ACC AAC ACA AGA AGG GGA ACT GGC AAC ATA GGA GAG ACG CTT GGA GAG Thr Asn Thr Arg Arg Gly Thr Gly Asn Ile Gly Glu Thr Leu Gly Glu 2490 2495 2500	7602
AAA TGG AAA AGC CGA TTG AAC GCA TTG GGA AAA AGT GAA TTC CAG ATC Lys Trp Lys Ser Arg Leu Asn Ala Leu Gly Lys Ser Glu Phe Gln Ile 2505 2510 2515	7650
TAC AAG AAA AGT GGA ATC CAG GAA GTG GAT AGA ACC TTA GCA AAA GAA Tyr Lys Lys Ser Gly Ile Gln Glu Val Asp Arg Thr Leu Ala Lys Glu 2520 2525 2530	7698
GGC ATT AAA AGA GGA GAA ACG GAC CAT CAC GCT GTG TCG CGA GGC TCA Gly Ile Lys Arg Gly Glu Thr Asp His His Ala Val Ser Arg Gly Ser 2535 2540 2545 2550	7746
GCA AAA CTG AGA TGG TTC GTT GAG AGA AAC ATG GTC ACA CCA GAA GGG Ala Lys Leu Arg Trp Phe Val Glu Arg Asn Met Val Thr Pro Glu Gly 2555 2560 2565	7794
AAA GTA GTG GAC CTC GGT TGT GGC AGA GGA GGC TGG TCA TAC TAT TGT Lys Val Val Asp Leu Gly Cys Gly Arg Gly Gly Trp Ser Tyr Tyr Cys 2570 2575 2580	7842
GGA GGA CTA AAG AAT GTA AGA GAA GTC AAA GGC CTA ACA AAA GGA GGA Gly Gly Leu Lys Asn Val Arg Glu Val Lys Gly Leu Thr Lys Gly Gly 2585 2590 2595	7890

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CCA GGA CAC GAA GAA CCC ATC CCC ATG TCA ACA TAT GGG TGG AAT CTA Pro Gly His Glu Glu Pro Ile Pro Met Ser Thr Tyr Gly Trp Asn Leu 2600 2605 2610	7938
GTG CGT CTT CAA AGT GGA GTT GAC GTT TTC TTC ATC CCG CCA GAA AAG Val Arg Leu Gln Ser Gly Val Asp Val Phe Phe Ile Pro Pro Glu Lys 2615 2620 2625 2630	7986
TGT GAC ACA TTA TTG TGT GAC ATA GGG GAG TCA TCA CCA AAT CCC ACA Cys Asp Thr Leu Leu Cys Asp Ile Gly Glu Ser Ser Pro Asn Pro Thr 2635 2640 2645	8034
GTG GAA GCA GGA CGA ACA CTC AGA GTC CTT AAC TTA GTA GAA AAT TGG Val Glu Ala Gly Arg Thr Leu Arg Val Leu Asn Leu Val Glu Asn Trp 2650 2655 2660	8082
TTG AAC AAC AAC ACT CAA TTT TGC ATA AAG GTT CTC AAC CCA TAT ATG Leu Asn Asn Asn Thr Gln Phe Cys Ile Lys Val Leu Asn Pro Tyr Met 2665 2670 2675	8130
CCC TCA GTC ATA GAA AAA ATG GAA GCA CTA CAA AGG AAA TAT GGA GGA Pro Ser Val Ile Glu Lys Met Glu Ala Leu Gln Arg Lys Tyr Gly Gly 2680 2685 2690	8178
GCC TTA GTG AGG AAT CCA CTC TCA CGA AAC TCC ACA CAT GAG ATG TAC Ala Leu Val Arg Asn Pro Leu Ser Arg Asn Ser Thr His Glu Met Tyr 2695 2700 2705 2710	8226
TGG GTA TCC AAT GCT TCC GGG AAC ATA GTG TCA TCA GTG AAC ATG ATT Trp Val Ser Asn Ala Ser Gly Asn Ile Val Ser Ser Val Asn Met Ile 2715 2720 2725	8274
TCA AGG ATG TTG ATC AAC AGA TTT ACA ATG AGA TAC AAG AAA GCC ACT Ser Arg Met Leu Ile Asn Arg Phe Thr Met Arg Tyr Lys Lys Ala Thr 2730 2735 2740	8322
TAC GAG CCG GAT GTT GAC CTC GGA AGC GGA ACC CGT AAC ATC GGG ATT Tyr Glu Pro Asp Val Asp Leu Gly Ser Gly Thr Arg Asn Ile Gly Ile 2745 2750 2755	8370
GAA AGT GAG ATA CCA AAC CTA GAT ATA ATT GGG AAA AGA ATA GAA AAA Glu Ser Glu Ile Pro Asn Leu Asp Ile Ile Gly Lys Arg Ile Glu Lys 2760 2765 2770	8418
ATA AAG CAA GAG CAT GAA ACA TCA TGG CAC TAT GAC CAA GAC CAC CCA Ile Lys Gln Glu His Glu Thr Ser Trp His Tyr Asp Gln Asp His Pro 2775 2780 2785 2790	8466
TAC AAA ACG TGG GCA TAC CAT GGT AGC TAT GAA ACA AAA CAG ACT GGA Tyr Lys Thr Trp Ala Tyr His Gly Ser Tyr Glu Thr Lys Gln Thr Gly 2795 2800 2805	8514
TCA GCA TCA TCC ATG GTC AAC GGA GTG GTC AGG CTG CTG ACA AAA CCT Ser Ala Ser Ser Met Val Asn Gly Val Val Arg Leu Leu Thr Lys Pro 2810 2815 2820	8562
TGG GAC GTT GTC CCC ATG GTG ACA CAG ATG GCA ATG ACA GAC ACG ACT Trp Asp Val Val Pro Met Val Thr Gln Met Ala Met Thr Asp Thr Thr 2825 2830 2835	8610

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CCA TTT GGA CAA CAG CGC GTT TTT AAA GAG AAA GTG GAC ACG AGA ACC Pro Phe Gly Gln Gln Arg Val Phe Lys Glu Lys Val Asp Thr Arg Thr 2840 2845 2850	8658
CAA GAA CCG AAA GAA GGC ACG AAG AAA CTA ATG AAA ATA ACA GCA GAG Gln Glu Pro Lys Glu Gly Thr Lys Lys Leu Met Lys Ile Thr Ala Glu 2855 2860 2865 2870	8706
TGG CTT TGG AAA GAA TTA GGG AAG AAA AAG ACA CCC AGG ATG TGC ACC Trp Leu Trp Lys Glu Leu Gly Lys Lys Lys Thr Pro Arg Met Cys Thr 2875 2880 2885	8754
AGA GAA GAA TTC ACA AGA AAG GTG AGA AGC AAT GCA GCC TTG GGG GCC Arg Glu Glu Phe Thr Arg Lys Val Arg Ser Asn Ala Ala Leu Gly Ala 2890 2895 2900	8802
ATA TTC ACT GAT GAG AAC AAG TGG AAG TCG GCA CGT GAG GCT GTT GAA Ile Phe Thr Asp Glu Asn Lys Trp Lys Ser Ala Arg Glu Ala Val Glu 2905 2910 2915	8850
GAT AGT AGG TTT TGG GAG CTG GTT GAC AAG GAA AGG AAT CTC CAT CTT Asp Ser Arg Phe Trp Glu Leu Val Asp Lys Glu Arg Asn Leu His Leu 2920 2925 2930	8898
GAA GGA AAG TGT GAA ACA TGT GTG TAC AAC ATG ATG GGA AAA AGA GAG Glu Gly Lys Cys Glu Thr Cys Val Tyr Asn Met Met Gly Lys Arg Glu 2935 2940 2945 2950	8946
AAG AAG CTA GGG GAA TTC GGC AAG GCA AAA GGC AGC AGA GCC ATA TGG Lys Lys Leu Gly Glu Phe Gly Lys Ala Lys Gly Ser Arg Ala Ile Trp 2955 2960 2965	8994
TAC ATG TGG CTT GGA GCA CGC TTC TTA GAG TTT GAA GCC CTA GGA TTC Tyr Met Trp Leu Gly Ala Arg Phe Leu Glu Phe Glu Ala Leu Gly Phe 2970 2975 2980	9042
TTA AAT GAA GAT CAC TGG TTC TCC AGA GAG AAC TCC CTG AGT GGA GTG Leu Asn Glu Asp His Trp Phe Ser Arg Glu Asn Ser Leu Ser Gly Val 2985 2990 2995	9090
GAA GGA GAA GGG CTG CAC AAG CTA GGT TAC ATT CTA AGA GAC GTG AGC Glu Gly Glu Gly Leu His Lys Leu Gly Tyr Ile Leu Arg Asp Val Ser 3000 3005 3010	9138
AAG AAA GAG GGA GGA GCA ATG TAT GCC GAT GAC ACC GCA GGA TGG GAT Lys Lys Glu Gly Gly Ala Met Tyr Ala Asp Asp Thr Ala Gly Trp Asp 3015 3020 3025 3030	9186
ACA AGA ATC ACA CTA GAA GAC KKA AAA AAT GAA GAA ATG GTA ACA AAC Thr Arg Ile Thr Leu Glu Asp Xaa Lys Asn Glu Glu Met Val Thr Asn 3035 3040 3045	9234
CAC ATG GAA GGA GAA CAC AAG AAA CTA GCC GAG GCC ATT TTC AAA CTA His Met Glu Gly Glu His Lys Lys Leu Ala Glu Ala Ile Phe Lys Leu 3050 3055 3060	9282
ACG TAC CAA AAC AAG GTG GTG CGT GTG CAA AGA CCA ACA CCA AGA GGC Thr Tyr Gln Asn Lys Val Val Arg Val Gln Arg Pro Thr Pro Arg Gly 3065 3070 3075	9330

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ACA GTA ATG GAC ATC ATA TCG AGA AGA GAC CAA AGA GGT AGT GGA CAA Thr Val Met Asp Ile Ile Ser Arg Arg Asp Gln Arg Gly Ser Gly Gln 3080 3085 3090	9378
GTT GGC ACC TAT GGA CTC AAT ACT TTC ACC AAT ATG GAA GCC CAA CTA Val Gly Thr Tyr Gly Leu Asn Thr Phe Thr Asn Met Glu Ala Gln Leu 3095 3100 3105 3110	9426
ATC AGA CAG ATG GAG GGA GAA GGA GTC TTT AAA AGC ATT CAG CAC CTA Ile Arg Gln Met Glu Gly Glu Gly Val Phe Lys Ser Ile Gln His Leu 3115 3120 3125	9474
ACA ATC ACA GAA GAA ATC GCT GTG CAA AAC TGG TTA GCA AGA GTG GGG Thr Ile Thr Glu Glu Ile Ala Val Gln Asn Trp Leu Ala Arg Val Gly 3130 3135 3140	9522
CGC GAA AGG TTA TCA AGA ATG GCC ATC AGT GGA GAT GAT TGT GTT GTG Arg Glu Arg Leu Ser Arg Met Ala Ile Ser Gly Asp Asp Cys Val Val 3145 3150 3155	9570
AAA CCT TTA GAT GAC AGG TTC GCA AGC GCT TTA ACA GCT CTA AAT GAC Lys Pro Leu Asp Asp Arg Phe Ala Ser Ala Leu Thr Ala Leu Asn Asp 3160 3165 3170	9618
ATG GGA AAG ATT AGG AAA GAC ATA CAA CAA TGG GAA CCT TCA AGA GGA Met Gly Lys Ile Arg Lys Asp Ile Gln Gln Trp Glu Pro Ser Arg Gly 3175 3180 3185 3190	9666
TGG AAT GAT TGG ACA CAA GTG CCC TTC TGT TCA CAC CAT TTC CAT GAG Trp Asn Asp Trp Thr Gln Val Pro Phe Cys Ser His His Phe His Glu 3195 3200 3205	9714
TTA ATC ATG AAA GAC GGT CGC GTA CTC GTT GTT CCA TGT AGA AAC CAA Leu Ile Met Lys Asp Gly Arg Val Leu Val Val Pro Cys Arg Asn Gln 3210 3215 3220	9762
GAT GAA CTG ATT GGC AGA GCC CGA ATC TCC CAA GGA GCA GGG TGG TCT Asp Glu Leu Ile Gly Arg Ala Arg Ile Ser Gln Gly Ala Gly Trp Ser 3225 3230 3235	9810
TTG CGG GAG ACG GCC TGT TTG GGG AAG TCT TAC GCC CAA ATG TGG AGC Leu Arg Glu Thr Ala Cys Leu Gly Lys Ser Tyr Ala Gln Met Trp Ser 3240 3245 3250	9858
TTG ATG TAC TTC CAC AGA CGC GAC CTC AGG CTG GCG GCA AAT GCT ATT Leu Met Tyr Phe His Arg Arg Asp Leu Arg Leu Ala Ala Asn Ala Ile 3255 3260 3265 3270	9906
TGC TCG GCA GTA CCA TCA CAT TGG GTT CCA ACA AGT CGA ACA ACC TGG Cys Ser Ala Val Pro Ser His Trp Val Pro Thr Ser Arg Thr Thr Trp 3275 3280 3285	9954
TCC ATA CAT GCT AAA CAT GAA TGG ATG ACA ACG GAA GAC ATG CTG ACA Ser Ile His Ala Lys His Glu Trp Met Thr Thr Glu Asp Met Leu Thr 3290 3295 3300	10002
GTC TGG AAC AGG GTG TGG ATT CAA GAA AAC CCA TGG ATG GAA GAC AAA Val Trp Asn Arg Val Trp Ile Gln Glu Asn Pro Trp Met Glu Asp Lys 3305 3310 3315	10050

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ACT CCA GTG GAA TCA TGG GAG GAA ATC CCA TAC TTG GGG AAA AGA GAA 10098
 Thr Pro Val Glu Ser Trp Glu Glu Ile Pro Tyr Leu Gly Lys Arg Glu
 3320 3325 3330

GAC CAA TGG TGC GGC TCA TTG ATT GGG TTA ACA AGC AGG GCC ACC TGG 10146
 Asp Gln Trp Cys Gly Ser Leu Ile Gly Leu Thr Ser Arg Ala Thr Trp
 3335 3340 3345 3350

GCA AAG AAC ATC CAA GCA GCA ATA AAT CAA GTT AGA TCC CTT ATA GGC 10194
 Ala Lys Asn Ile Gln Ala Ala Ile Asn Gln Val Arg Ser Leu Ile Gly
 3355 3360 3365

AAT GAA GAA TAC ACA GAT TAC ATG CCA TCC ATG AAA AGA TTC AGA AGA 10242
 Asn Glu Glu Tyr Thr Asp Tyr Met Pro Ser Met Lys Arg Phe Arg Arg
 3370 3375 3380

GAA GAG GAA GAA GCA GGA GTT CTG TGG TAGAAAGCAA AACTAACATG AAACAAGG 10297
 Glu Glu Glu Glu Ala Gly Val Leu Trp
 3385 3390

CTAGAAGTCA GGTCCGATTA AGCCATAGTA CGGAAAAAAC TATGCTACCT GTGAGCCCCG 10357
 TCCAAGGACG TTAAAAGAAG TCAGGCCATC ATAAATGCCA TAGCTTGAGT AAACATATGCA 10417
 GCCTGTAGCT CCACCTGAGA AGGTGTAAAA AATCCGGGAG GCCACAAACC ATGGAAGCTG 10477
 TACGCATGGC GTAGTGGACT AGCGGTTAGA GAGGACCCCT CCCTTACAAA TCGCAGCAAC 10537
 AATGGGGGCC CAAGGCGAGA TGAAGCTGTA GTCTCGCTGG AAGGACTAGA GGTAGAGGA 10597
 GACCCCCCG AAACAAAAAA CAGCATATTG ACGCTGGGAA AGACCAGAGA TCCTGCTGTC 10657
 TCCTCAGCAT CATTCAGGC ACAGAACGCC AGAAAATGGA ATGGTGCTGT TGAATCAACA 10717
 GGTTCCT 10723

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCAGTCACG ACGTTGTAAC ACGAC

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

137

GGATGTGCTG CAAGGCGATT AAGTTGG

27

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGAGCGGATA ACAATTCAC ACAGG

25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCTTTACAC TTTATGCTTC CGGCTCG

27

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGGATATTG GAATTCTCTA GAAATTTAAT ACGACTCACT ATAAGTTGTT AGTCTACGTG
GACCGACAAA GACAG60
75

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCAGTGAATT CGAGCTCACG CGTAAATTTA ATACGACTCA CTATAAGTTG TTAGTCTACG
TGGACCGACA AAGACAG

60
77

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGTTGTTAGT CTACGTGGAC CGAC

24

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GACAGATTCT TTGAGGGAGC TGAGCTCAAC GTAG

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(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCAATATGCT GAAACGCGAG AGAAACCG

28

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGATTGTTA GGAAACGAAG GAACGC

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCACCAACAG CAGGGATACT GAAAAGATGG GG

32

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

1.40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCAGATCTG CGTCTCCTAT TCAAG

25

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGTGAACATG TGTACCCTCA TGGCC

25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTGCACCAAC AGTCAATGTC TTCAGG

26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACCAGAAGAC ATAGATTGTT GGTGC

25

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

141

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCACCAACAG TCTATGTCTT CTGGC

25

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGTTTCCAG GCCCCTTCTG ATGAC

25

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCAGCAATCC TGGCATACAC CATAG

25

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

142

- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGTTGACATA GTCTTAGAAC ATGGAAG

27

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTTCCATGTT CTAAGACTAT GTCAACC

27

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCTTAGAAC ATGGAAGTTG TGTGACGACG ATGGC

35

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACAACAGAAT CTCGCTGCCC AACAC

25

143

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCAAACACTC CATGGTAGAC AGAGG

25

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCTCTGTCTA CCATGGAGTG TTTGC

25

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCACATCCAT TTCCCCATCC TCTGTCT

27

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

144

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGAAAGGGAG GCATTGTGAC CTGTGCTATG

30

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGAAATCAAA ATAACACCAC AGAGTTCC

28

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTGCAGCAAC ACCATCTCAT TGAAGTCGAG GCCC

34

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GACTTCAATG AGATGGTGCT GCTGC

25

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCAGCAGCAC CATCTCATTG AAGTC

25

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AAGCTTGGCT GGTGCACAGG CAATGGTT

28

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TGGTAACGGC AGGTCTAGGA ACCATTG

27

(2) INFORMATION FOR SEQ ID NO:35:

146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGACATCTCA AGTGCAGGCT GAG

23

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTCAGCCTGC ACTTGAGATG TCC

23

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAAGGAAATA GCAGAAACAC AACATGG

27

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

147

(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCCTTCATAT TGTACTCTGA TAACTATTGT TCC

33

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCTCCATTCG GAGACAGCTA CATCATCATA GG

32

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCTATGATGA TG TAGCTGTC TCCGAATGGA GG

32

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGGCCATTT TAGGTGACAC AGCCTGGGA

29

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TGTAACACT CCTCCCAGGG ATCCAAA

27

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCATAGGAG TCATTATCAC ATGGATAGG

29

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGGGATTCTG GTTGGAACCTT ATATTGTTCT GTCC

34

(2) INFORMATION FOR SEQ ID NO:45:

149

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGATTCAATT CTGGTGTTAT TTGTTTCCAC

30

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AAGGAATCAT GCAGGCAGGA AAACG

25

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACTTCCAGCG AGTTCCAAGC TC

22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

150.

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AACAGAGCCG TCCATGCCGA TATGG

25

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TCCATTGCTC CAAAGGGTGT GT

22

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGCTTGAGAT GGACTTTGAT TTCTG

25

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGTCTGATTT CCATCCCGTA CC

22

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTCCTTTAGA GACCTGGGAA GAG

23

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GTTTTCTCAA GAGTAGTCCA GCTGC

25

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATCAATTGGC AGTGACTATC ATGGC

25

(2) INFORMATION FOR SEQ ID NO:55:

152

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TGTTAAGAGC AGTGGAGAAA CGGAC

25

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GATTGAGACC TTTGATCGTC AACGC

25

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGACAGGACC ATTAGTGGCT GGAGG

25

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

153

(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CGTGCTCACT GGACGATCGG CCGATTGGA ACTG

34

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGGCTGCTTC CTGATATTTT TGCC

24

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCTGTGGGAA GTGAAGAAAC AACGG

25

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GCTCCATCTT CCAGTTCAGC CTTTCCCATG

30

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTCCGGCTCC AATCTGAGAG TATCC

25

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCTAATATCA TATGGAGGAG GCTGG

25

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GAAGGAGAAG AAGTCCAGGT ATTGG

25

(2) INFORMATION FOR SEQ ID NO:65:

155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTGTCGACAA TTGGAGATCC TGACG

25

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTGGAGCATA TGTGAGTGCT ATAGC

25

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TCTGACTATG GCCGGAAGGT ATCTC

25

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

156

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACATTAATCT TGGCCCCAC TAGAG

25

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CGATCTCCCG CCCGGTGTG

19

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTAACTGGTG ATAGCAGCCT CATGG

25

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CCTACTGAGT TGTATCACTT TCTTTCC

27

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGGATTCTT CCTATTCTCC CTCTTC

26

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TTCAAGGCTG AGAGGGTTAT AGACC

25

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TCTGGTTGGC CTACAGAGTG GCAGC

25

(2) INFORMATION FOR SEQ ID NO:75:

158

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCTTCTTTTG TCCAGATTTC CACTTCC

27

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GCGTACAACC ATGCTCTCAG TGAAGTGGCCG GAGAC

35

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TTCCCAGGGT CATCTTCCCT ATAC

24

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

159

(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GATGCTAGCC GTGATTATGC AGCACATTCC C

31

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AAACAGAGAA CACCCAAGA CAACC

25

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CGGCATACAG CGTCCATGCT G

21

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GTCTCGGGAA AGGATGGCCA TTGTC

25

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTCTGGTTGC TTTTGCTTGA AGTCC

25

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCGCCGCTGC TCTTTTCTGA GCTTCTC

27

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

AGGACTACAT GGGCTCTGTG TGAGG

25

(2) INFORMATION FOR SEQ ID NO:85:

161

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGAAGTCCA GCTCCGGCC

19

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AGAGAAACAT GGTCACACCA GAAGG

25

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTTCTTCGTG TCCTGGTCCT CC

22

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

162

(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GGAAATATGG AGGAGCCTAG TGAGG

25

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ACCCAGTACA TCTCATGTGT GG

22

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GAGCATGAAA CATCATGGCA CTATGACC

28

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCATGGCACT ATGACCAAGA CCACC

25

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CAGTCTGACC ACTCCGTTCA CC

22

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

AAGGTGAGAA GCAATGCAGC CTTGG

25

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GGGCCATATT CACTGATGAG AACAAAGTGG

29

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

164

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCTTTCCCTG TCAACCAGCT CC

22

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

AATGAAGATC ACTGGTTCTC CAGAG

25

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACGTGAGCAA GAAAGAGGGA GGAGC

25

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

165.

- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TGTCCCATCC TGCTGTGTCA TC

22

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GCTAGTTTCT TGTGTTCTCC TTCCATGTGG

30

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TCATATCGAG AAGAGACCAA AGAGG

25

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

ACTCCTTCTC CCTCCATCTG TCTG

24

166

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATGCTTTTGA AGATTCCTTC TCCCTCC

27

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCACAGCGAT TTCTTCTGTG ATTGTTAGGT GC

32

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ACAATGGGAA CCTTCAAGAG GATGG

25

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

167

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTATCACATT GGATCCTTCA AGAGGATGGA ATGATTGGAC ACAAG

45

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CAGAAGGGCA CTTGTGTCCA ATCATTCC

28

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTCCCTGGGA AATTCGGGCT C

21

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CCGTCTCCCG CAAAGACCAC CCTGCTCC

28

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TTATCACCTA TCTAGACCGT CTCCGCAAA GACCACCCTG CTCC

44

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTTGAACCC AATGTGATGG TACTGC

26

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ACAAGTCGAA CAACCTGGTC CATAC

25

(2) INFORMATION FOR SEQ ID NO:112:

169

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GCATGTCTTC CGTCGTCATC C

21

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTTGAATCCA CACCCTGTTC CAGAC

25

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

ATACACAGAT TACATGCCAT CCATG

25

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

170

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TTTTCCTTC TACCACAGGA C

21

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAAACAAGGC TAGAAGTCAG GTCGG

25

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GACGGGGCTC ACAGGTAGCA TAG

23

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCCTGTAGCT CCACCTGAGA AGGTG

25

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GGAAGCTGTA CGCATGGCGT AGTGG

25

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GGGCCCCCGT TGTTGCTGC

19

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

AGAACCTGTT GATTCAACAG CACCATTCCA TTTTCTG

37

(2) INFORMATION FOR SEQ ID NO:122:

172

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TTATCACCTA GCATGCTCTA GAAGAACCTG TTGATTCAAC AGCACCATTC CATTTTCTG

59

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TTATCACCTA TCTAGAGAAC CTGTTGATTC AACAGCACCA TTCCATTTTC TG

52

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2394

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

AGA TTC TCA AAA GGA TTG CTC TCA GGC CAA GGA CCC ATG AAA TTG GTG
 Arg Phe Ser Lys Gly Leu Leu Ser Gly Gln Gly Pro Met Lys Leu Val
 1 5 10 15

48

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ATG	GCT	TTC	ATA	GCA	TTC	TTA	AGA	TTT	CTA	GCC	ATA	CCC	CCA	ACA	GCA	96
Met	Ala	Phe	Ile	Ala	Phe	Leu	Arg	Phe	Leu	Ala	Ile	Pro	Pro	Thr	Ala	
			20					25					30			
GGA	ATT	TTG	GCT	AGA	TGG	GGC	TCA	TTC	AAG	AAG	AAT	GGA	GCG	ATT	AAA	144
Gly	Ile	Leu	Ala	Arg	Trp	Gly	Ser	Phe	Lys	Lys	Asn	Gly	Ala	Ile	Lys	
		35				40						45				
GTG	TTA	CGG	GGT	TTC	AAG	AGA	GAA	ATC	TCA	AAC	ATG	CTA	AAC	ATA	ATG	192
Val	Leu	Arg	Gly	Phe	Lys	Arg	Glu	Ile	Ser	Asn	Met	Leu	Asn	Ile	Met	
	50					55					60					
AAC	AGG	AGG	AAA	AGA	TCC	GTG	ACC	ATG	CTC	CTT	ATG	CTG	CTG	CCC	ACA	240
Asn	Arg	Arg	Lys	Arg	Ser	Val	Thr	Met	Leu	Leu	Met	Leu	Leu	Pro	Thr	
65					70				75						80	
GCC	CTG	GCG	TTC	CAT	CTG	ACG	ACA	CGA	GGG	GGA	GAG	CCG	CAT	ATG	ATA	288
Ala	Leu	Ala	Phe	His	Leu	Thr	Thr	Arg	Gly	Gly	Glu	Pro	His	Met	Ile	
				85					90					95		
GTT	AGC	AAG	CAG	GAA	AGA	GGA	AAG	TCA	CTT	TTG	TTC	AAG	ACC	TCT	GCA	336
Val	Ser	Lys	Gln	Glu	Arg	Gly	Lys	Ser	Leu	Leu	Phe	Lys	Thr	Ser	Ala	
			100					105					110			
GGT	GTC	AAC	ATG	TGC	ACC	CTC	ATT	GCG	ATG	GAT	TTG	GGA	GAG	TTG	TGT	384
Gly	Val	Asn	Met	Cys	Thr	Leu	Ile	Ala	Met	Asp	Leu	Gly	Glu	Leu	Cys	
		115					120					125				
GAG	GAC	ACG	ATG	ACC	TAC	AAA	TGC	CCC	CGG	ATC	ACT	GAG	GCG	GAA	CCA	432
Glu	Asp	Thr	Met	Thr	Tyr	Lys	Cys	Pro	Arg	Ile	Thr	Glu	Ala	Glu	Pro	
	130					135					140					
GAT	GAC	GTT	GAC	TGT	TGG	TGC	AAT	GCC	ACG	GAC	ACA	TGG	GTG	ACC	TAT	480
Asp	Asp	Val	Asp	Cys	Trp	Cys	Asn	Ala	Thr	Asp	Thr	Trp	Val	Thr	Tyr	
145				150						155					160	
GGA	ACG	TGC	TCT	CAA	ACT	GGC	GAA	CAC	CGA	CGA	GAC	AAA	CGT	TCC	GTC	528
Gly	Thr	Cys	Ser	Gln	Thr	Gly	Glu	His	Arg	Arg	Asp	Lys	Arg	Ser	Val	
				165					170					175		
GCA	TTG	GCC	CCA	CAC	GTG	GGG	CTT	GGC	CTA	GAA	ACA	AGA	GCC	GAA	ACG	576
Ala	Leu	Ala	Pro	His	Val	Gly	Leu	Gly	Leu	Glu	Thr	Arg	Ala	Glu	Thr	
			180					185					190			
TGG	ATG	TCC	TCT	GAA	GGT	GCT	TGG	AAA	CAG	ATA	CAA	AAA	GTA	GAG	ACT	624
Trp	Met	Ser	Ser	Glu	Gly	Ala	Trp	Lys	Gln	Ile	Gln	Lys	Val	Glu	Thr	
		195					200					205				
TGG	GCT	CTG	AGA	CAT	CCA	GGA	TTC	ACG	GTG	ATA	GCC	CTT	TTT	CTA	GCA	672
Trp	Ala	Leu	Arg	His	Pro	Gly	Phe	Thr	Val	Ile	Ala	Leu	Phe	Leu	Ala	
	210					215					220					
CAT	GCC	ATA	GGA	ACA	TCC	ATC	ACC	CAG	AAA	GGG	ATC	ATT	TTC	ATT	TTG	720
His	Ala	Ile	Gly	Thr	Ser	Ile	Thr	Gln	Lys	Gly	Ile	Ile	Phe	Ile	Leu	
225					230					235					240	
CTG	ATG	CTG	GTA	ACA	CCA	TCT	ATG	GCC	ATG	CGA	TGC	GTG	GGA	ATA	GGC	768
Leu	Met	Leu	Val	Thr	Pro	Ser	Met	Ala	Met	Arg	Cys	Val	Gly	Ile	Gly	
				245					250					255		

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AAC Asn	AGA Arg	GAC Asp	TTC Phe 260	GTG Val	GAA Glu	GGA Gly	CTG Leu	TCA Ser 265	GGA Gly	GCA Ala	ACA Thr	TGG Trp 270	GTG Val	GAT Asp	GTG Val	816
GTA Val	CTG Leu	GAG Glu 275	CAT His	GGA Gly	AGT Ser	TGC Cys	GTC Val 280	ACC Thr	ACC Thr	ATG Met	GCA Ala	AAA Lys 285	AAC Asn	AAA Lys	CCA Pro	864
ACA Thr 290	CTG Leu	GAC Asp	ATT Ile	GAA Glu	CTC Leu	TTG Leu 295	AAG Lys	ACG Thr	GAG Glu	GTC Val 300	ACA Thr	AAC Asn	CCT Pro	GCA Ala	GTT Val	912
CTG Leu 305	CGT Arg	AAA Lys	TTG Leu	TGC Cys	ATT Ile 310	GAA Glu	GCT Ala	AAA Lys	ATA Ile 315	TCA Ser	AAC Asn	ACC Thr	ACC Thr	ACC Thr	GAT Asp 320	960
TCG Ser	AGA Arg	TGT Cys	CCA Pro 325	ACA Thr	CAA Gln	GGA Gly	GAA Glu	GCC Ala	ACA Thr 330	CTG Leu	GTG Val	GAA Glu	GAA Glu	CAA Gln 335	GAC Asp	1008
GCG Ala	AAC Asn	TTT Phe 340	GTG Val	TGC Cys	CGA Arg	CGA Arg	ACG Thr	TTC Phe 345	GTG Val	GAC Asp	AGA Arg	GGC Gly	TGG Trp 350	GGC Gly	AAT Asn	1056
GGC Gly	TGT Cys	GGG Gly 355	CTA Leu	TTC Phe	GGA Gly	AAA Lys	GGT Gly 360	AGT Ser	CTA Leu	ATA Ile	ACG Thr	TGT Cys 365	GCC Ala	AAG Lys	TTT Phe	1104
AAG Lys 370	TGT Cys	GTG Val	ACA Thr	AAA Lys	CTA Leu	GAA Glu 375	GGA Gly	AAG Lys	ATA Ile	GCT Ala	CAA Gln 380	TAT Tyr	GAA Glu	AAC Asn	CTA Leu	1152
AAA Lys 385	TAT Tyr	TCA Ser	GTG Val	ATA Ile	GTC Val 390	ACC Thr	GTC Val	CAC His	ACT Thr	GGA Gly 395	GAT Asp	CAG Gln	CAC His	CAG Gln	GTG Val 400	1200
GGA Gly	AAT Asn	GAG Glu	ACT Thr 405	ACA Thr	GAA Glu	CAT His	GGA Gly	ACA Thr 410	ACT Thr	GCA Ala	ACC Thr	ATA Ile	ACA Thr 415	CCT Pro	CAA Gln	1248
GCT Ala	CCT Pro	ACG Thr 420	TCG Ser	GAA Glu	ATA Ile	CAG Gln	CTG Leu	ACC Thr 425	GAC Asp	TAC Tyr	GGA Gly	ACC Thr	CTT Leu 430	ACA Thr	TTA Leu	1296
GAT Asp	TGT Cys	TCA Ser 435	CCT Pro	AGG Arg	ACA Thr	GGG Gly	CTA Leu 440	GAT Asp	TTT Phe	AAC Asn	GAG Glu	ATG Met 445	GTG Val	TTG Leu	CTG Leu	1344
ACA Thr 450	ATG Met	AAA Lys	AAG Lys	AAA Lys	TCA Ser	TGG Trp 455	CTT Leu	GTC Val	CAC His	AAA Lys	CAG Gln 460	TGG Trp	TTT Phe	CTA Leu	GAC Asp	1392
TTA Leu 465	CCA Pro	CTG Leu	CCT Pro	TGG Trp	ACC Thr 470	TCT Ser	GGG Gly	GCT Ala	TTA Leu 475	ACA Thr	TCC Ser	CAA Gln	GAG Glu	ACT Thr	TGG Trp 480	1440
AAC Asn	AGA Arg	CAA Gln	GAT Asp 485	TTA Leu	CTG Leu	GTC Val	ACA Thr	TTT Phe 490	AAG Lys	ACA Thr	GCT Ala	CAT His	GCA Ala	AAG Lys 495	AAG Lys	1488

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CAG GAA GTA GTC GTA CTA GGA TCA CAA GAA GGA GCA ATG CAC ACT GCG Gln Glu Val Val Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala 500 505 510	1536
CTG ACT GGA GCG ACA GAA ATC CAA ACG TCA GGA ACG ACA ACA ATT TTC Leu Thr Gly Ala Thr Glu Ile Gln Thr Ser Gly Thr Thr Thr Ile Phe 515 520 525	1584
GCA GGA CAC CTA AAA TGC AGA CTA AAA ATG GAC AAA CTA ACT TTA AAA Ala Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Thr Leu Lys 530 535 540	1632
GGG ATG TCA TAT GTG ATG TGC ACA GGC TCA TTC AAG TTA GAG AAA GAA Gly Met Ser Tyr Val Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu 545 550 555 560	1680
GTG GCT GAG ACC CAG CAT GGA ACT GTT CTG GTG CAG GTT AAA TAT GAA Val Ala Glu Thr Gln His Gly Thr Val Leu Val Gln Val Lys Tyr Glu 565 570 575	1728
GGA ACA GAC GCA CCA TGC AAG ATT CCC TTT TCG ACC CAA GAT GAG AAA Gly Thr Asp Ala Pro Cys Lys Ile Pro Phe Ser Thr Gln Asp Glu Lys 580 585 590	1776
GGA GCA ACC CAG AAT GGG AGA TTA ATA ACA GCC AAC CCC ATA GTC ACT Gly Ala Thr Gln Asn Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr 595 600 605	1824
GAC AAA GAA AAA CCA GTC AAT ATT GAG GCA GAA CCA CCC TTT GGT GAG Asp Lys Glu Lys Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu 610 615 620	1872
AGC TAC ATC GTG GTA GGA GCA GGT GAA AAA GCT TTG AAA CTA AGC TGG Ser Tyr Ile Val Val Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp 625 630 635 640	1920
TTC AAG AAA GGA AGC AGC ATA GGG AAA ATG TTT GAA GCA ACT GCC CGA Phe Lys Lys Gly Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg 645 650 655	1968
GGA GCA CGA AGG ATG GCC ATT CTG GGA GAC ACC GCA TGG GAC TTC GGT Gly Ala Arg Arg Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly 660 665 670	2016
TCT ATA GGA GGA GTG TTC ACG TCT ATG GGA AAA CTG GTA CAC CAG GTT Ser Ile Gly Gly Val Phe Thr Ser Met Gly Lys Leu Val His Gln Val 675 680 685	2064
TTT GGA ACT GCA TAT GGA GTT TTG TTT AGC GGA GTT TCT TGG ACC ATG Phe Gly Thr Ala Tyr Gly Val Leu Phe Ser Gly Val Ser Trp Thr Met 690 695 700	2112
AAA ATA GGA ATA GGG ATT CTG CTG ACA TGG CTA GGA TTA AAT TCA AGG Lys Ile Gly Ile Gly Ile Leu Leu Thr Trp Leu Gly Leu Asn Ser Arg 705 710 715 720	2160
AAC ACG TCC CTT TCG GTG ATG TGC ATC GCA GTT GGC ATG GTC ACA CTG Asn Thr Ser Leu Ser Val Met Cys Ile Ala Val Gly Met Val Thr Leu 725 730 735	2208

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TAC CTA GGA GTC ATG GTT CAG GCA GAT TCG GGA TGT GTA ATC AAC TGG	2256
Tyr Leu Gly Val Met Val Gln Ala Asp Ser Gly Cys Val Ile Asn Trp	
740 745 750	
AAA GGC AGA GAA CTT AAA TGT GGA AGC GGC ATT TTT GTC ACT AAT GAA	2304
Lys Gly Arg Glu Leu Lys Cys Gly Ser Gly Ile Phe Val Thr Asn Glu	
755 760 765	
GTT CAC ACT TGG ACA GAG CAA TAC AAA TTC CAG GCT GAC TCC CCC AAG	2352
Val His Thr Trp Thr Glu Gln Tyr Lys Phe Gln Ala Asp Ser Pro Lys	
770 775 780	
AGA CTA TCA GCA GCC ATT GGG AAG GCA TGG GAG GAG GGT GTG	2394
Arg Leu Ser Ala Ala Ile Gly Lys Ala Trp Glu Gly Val	
785 790 795	

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2145

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

AAG GTC TTA AAA GGC TTC AAG AAG GAG ATC TCA AAC ATG CTG AGC ATT	48
Lys Val Leu Lys Gly Phe Lys Lys Glu Ile Ser Asn Met Leu Ser Ile	
1 5 10 15	
ATC AAC AAA CGG AAA AAG ACA TCG CTC TGT CTC ATG ATG ATG TTA CCA	96
Ile Asn Lys Arg Lys Lys Thr Ser Leu Cys Leu Met Met Met Leu Pro	
20 25 30	
GCA ACA CTT GCT TTC CAC TTA ACT TCA CGA GAT GGA GAG CCG CGC ATG	144
Ala Thr Leu Ala Phe His Leu Thr Ser Arg Asp Gly Glu Pro Arg Met	
35 40 45	
ATT GTG GGG AAG AAT GAA AGA GGA AAA TCC CTA CTT TTC AAG ACA GCC	192
Ile Val Gly Lys Asn Glu Arg Gly Lys Ser Leu Leu Phe Lys Thr Ala	
50 55 60	
TCT GGA ATC AAC ATG TGC ACA CTC ATA GCT ATG GAT CTG GGA GAG ATG	240
Ser Gly Ile Asn Met Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Met	
65 70 75 80	

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TGT GAT GAC ACG GTC ACT TAC AAA TGC CCC CAC ATT ACC GAA GTG GAG Cys Asp Asp Thr Val Thr Tyr Lys Cys Pro His Ile Thr Glu Val Glu	288
85 90	95
CCT GAA GAC ATT GAC TGC TGG TGC AAC CTT ACA TCG ACA TGG GTG ACT Pro Glu Asp Ile Asp Cys Trp Cys Asn Leu Thr Ser Thr Trp Val Thr	336
100 105	110
TAT GGA ACA TGC AAT CAA GCT GGA GAG CAT AGA CGC GAT AAG AGA TCA Tyr Gly Thr Cys Asn Gln Ala Gly Glu His Arg Arg Asp Lys Arg Ser	384
115 120	125
GTG GCG TTA GCT CCC CAT GTT GGC ATG GGA CTG GAC ACA CGC ACT CAA Val Ala Leu Ala Pro His Val Gly Met Gly Leu Asp Thr Arg Thr Gln	432
130 135	140
ACC TGG ATG TCG GCT GAA GGA GCT TGG AGA CAA GTC GAG AAG GTA GAG Thr Trp Met Ser Ala Glu Gly Ala Trp Arg Gln Val Glu Lys Val Glu	480
145 150	155 160
ACA TGG GCC CTT AGG CAC CCA GGG TTT ACC ATA CTA GCC CTA TTT CTT Thr Trp Ala Leu Arg His Pro Gly Phe Thr Ile Leu Ala Leu Phe Leu	528
165 170	175
GCC CAT TAC ATA GGC ACT TCC TTG ACC CAG AAA GTG GTT ATT TTT ATA Ala His Tyr Ile Gly Thr Ser Leu Thr Gln Lys Val Val Ile Phe Ile	576
180 185	190
CTA TTA ATG CTG GTT ACC CCA TCC ATG ACA ATG AGA TGT GTA GGA GTA Leu Leu Met Leu Val Thr Pro Ser Met Thr Met Arg Cys Val Gly Val	624
195 200	205
GGA AAC AGA GAT TTT GTG GAA GGC CTA TCG GGA GCT ACG TGG GTT GAC Gly Asn Arg Asp Phe Val Glu Gly Leu Ser Gly Ala Thr Trp Val Asp	672
210 215	220
GTG GTG CTC GAG CAC GGT GGG TGT GTG ACT ACC ATG GCT AAG AAC AAG Val Val Leu Glu His Gly Gly Cys Val Thr Thr Met Ala Lys Asn Lys	720
225 230	235 240
CCC ACG CTG GAC ATA GAG CTT CAG AAG ACC GAG GCC ACC CAA CTG GCG Pro Thr Leu Asp Ile Glu Leu Gln Lys Thr Glu Ala Thr Gln Leu Ala	768
245 250	255
ACC CTA AGG AAG CTA TGC ATT GAG GGA AAA ATT ACC AAC ATA ACA ACC Thr Leu Arg Lys Leu Cys Ile Glu Gly Lys Ile Thr Asn Ile Thr Thr	816
260 265	270
GAC TCA AGA TGT CCC ACC CAA GGG GAA GCG ATT TTA CCT GAG GAG CAG Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Ile Leu Pro Glu Glu Gln	864
275 280	285
GAC CAG AAC TAC GTG TGT AAG CAT ACA TAC GTG GAC AGA GGC TGG GGA Asp Gln Asn Tyr Val Cys Lys His Thr Tyr Val Asp Arg Gly Trp Gly	912
290 295	300
AAC GGT TGT GGT TTG TTT GGC AAG GGA AGC TTG GTG ACA TGC GCG AAA Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys	960
305 310	315 320

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TTT	CAA	TGT	TTA	GAA	TCA	ATA	GAG	GGA	AAA	GTG	GTG	CAA	CAT	GAG	AAC	1008
Phe	Gln	Cys	Leu	Glu	Ser	Ile	Glu	Gly	Lys	Val	Val	Gln	His	Glu	Asn	
				325					330					335		
CTC	AAA	TAC	ACC	GTC	ATC	ATC	ACA	GTG	CAC	ACA	GGA	GAC	CAA	CAC	CAG	1056
Leu	Lys	Tyr	Thr	Val	Ile	Ile	Thr	Val	His	Thr	Gly	Asp	Gln	His	Gln	
			340					345					350			
GTG	GGA	AAT	GAA	ACG	CAG	GGA	GTC	ACG	GCT	GAG	ATA	ACA	CCC	CAG	GCA	1104
Val	Gly	Asn	Glu	Thr	Gln	Gly	Val	Thr	Ala	Glu	Ile	Thr	Pro	Gln	Ala	
		355					360					365				
TCA	ACC	GCT	GAA	GCC	ATT	TTA	CCT	GAA	TAT	GGA	ACC	CTC	GGG	CTA	GAA	1152
Ser	Thr	Ala	Glu	Ala	Ile	Leu	Pro	Glu	Tyr	Gly	Thr	Leu	Gly	Leu	Glu	
	370					375					380					
TGC	TCA	CCA	CGG	ACA	GGT	TTG	GAT	TTC	AAT	GAA	ATG	ATC	TCA	TTG	ACA	1200
Cys	Ser	Pro	Arg	Thr	Gly	Leu	Asp	Phe	Asn	Glu	Met	Ile	Ser	Leu	Thr	
385					390					395					400	
ATG	AAG	AAC	AAA	GCA	TGG	ATG	GTA	CAT	AGA	CAA	TGG	TTC	TTT	GAC	TTA	1248
Met	Lys	Asn	Lys	Ala	Trp	Met	Val	His	Arg	Gln	Trp	Phe	Phe	Asp	Leu	
			405					410						415		
CCC	CTA	CCA	TGG	ACA	TCA	GGA	GCT	ACA	GCA	GAA	ACA	CCA	ACT	TGG	AAC	1296
Pro	Leu	Pro	Trp	Thr	Ser	Gly	Ala	Thr	Ala	Glu	Thr	Pro	Thr	Trp	Asn	
			420					425					430			
AGG	AAA	GAG	CTT	CTT	GTG	ACA	TTT	AAA	AAT	GCA	CAT	GCA	AAA	AAG	CAA	1344
Arg	Lys	Glu	Leu	Leu	Val	Thr	Phe	Lys	Asn	Ala	His	Ala	Lys	Lys	Gln	
		435					440					445				
GAA	GTA	GTT	GTT	CTT	GGA	TCA	CAA	GAG	GGA	GCA	ATG	CAT	ACA	GCA	CTG	1392
Glu	Val	Val	Val	Leu	Gly	Ser	Gln	Glu	Gly	Ala	Met	His	Thr	Ala	Leu	
	450					455					460					
ACA	GGA	GCT	ACA	GAG	ATC	CAA	ACC	TCA	GGA	GGC	ACA	AGT	ATC	TTT	GCG	1440
Thr	Gly	Ala	Thr	Glu	Ile	Gln	Thr	Ser	Gly	Gly	Thr	Ser	Ile	Phe	Ala	
465					470					475					480	
GGG	CAC	TTA	AAA	TGT	AGA	CTC	AAG	ATG	GAC	AAA	TTG	GAA	CTC	AAA	GGG	1488
Gly	His	Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Glu	Leu	Lys	Gly	
			485						490					495		
ATG	AGC	TAT	GCA	ATG	TGC	TTG	GGT	AGC	TTT	GTG	TTG	AAG	AAA	GAA	GTC	1536
Met	Ser	Tyr	Ala	Met	Cys	Leu	Gly	Ser	Phe	Val	Leu	Lys	Lys	Glu	Val	
			500					505					510			
TCC	GAA	ACG	CAG	CAT	GGG	ACA	ATA	CTC	ATT	AAG	GTT	GAG	TAC	AAA	GGG	1584
Ser	Glu	Thr	Gln	His	Gly	Thr	Ile	Leu	Ile	Lys	Val	Glu	Tyr	Lys	Gly	
		515					520					525				
AAA	GAT	GCA	CCC	TGC	AAG	ATT	CCT	TTC	TCC	ACG	GAG	GAT	GGA	CAA	GGA	1632
Lys	Asp	Ala	Pro	Cys	Lys	Ile	Pro	Phe	Ser	Thr	Glu	Asp	Gly	Gln	Gly	
	530					535					540					
AAA	GCT	CAC	AAT	GGC	AGA	CTG	ATC	ACA	GCC	AAT	CCA	GTG	GTG	ACC	AAG	1680
Lys	Ala	His	Asn	Gly	Arg	Leu	Ile	Thr	Ala	Asn	Pro	Val	Val	Thr	Lys	
545					550					555					560	

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AAG GAG GAG CCT GTC AAC ATT GAG GCT GAA CCT CCT TTT GGA GAA AGT	1728
Lys Glu Glu Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser	
565 570 575	
AAC ATA GTA ATT GGA ATT GGA GAC AAA GCC CTG AAA ATC AAC TGG TAC	1776
Asn Ile Val Ile Gly Ile Gly Asp Lys Ala Leu Lys Ile Asn Trp Tyr	
580 585 590	
AAG AAG GGA AGC TCG ATT GGG AAG ATG TTC GAG GCT ACT GCC AGA GGT	1824
Lys Lys Gly Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly	
595 600 605	
GCA AGG CGC ATG GCC ATC TTG GGA GAC ACA GCC TGG GAC TTT GGA TCA	1872
Ala Arg Arg Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser	
610 615 620	
GTG GGT GGT GTT TTG AAT TCA TTA GGG AAA ATG GTC CAC CAA ATA TTT	1920
Val Gly Gly Val Leu Asn Ser Leu Gly Lys Met Val His Gln Ile Phe	
625 630 635 640	
GGG AGT GCT TAC ACA GCC CTA TTT GGT GGA GTC TCC TGG ATG ATG AAA	1968
Gly Ser Ala Tyr Thr Ala Leu Phe Gly Gly Val Ser Trp Met Met Lys	
645 650 655	
ATT GGA ATA GGT GTC CTC TTA ACC TGG ATA GGG TTG AAC TCA AAA AAT	2016
Ile Gly Ile Gly Val Leu Leu Thr Trp Ile Gly Leu Asn Ser Lys Asn	
660 665 670	
ACT TCT ATG TCA TTT TCA TGC ATC GCG ATA GGA ATC ATT ACA CTC TAT	2064
Thr Ser Met Ser Phe Ser Cys Ile Ala Ile Gly Ile Ile Thr Leu Tyr	
675 680 685	
CTG GGA GCC GTG GTG CAA GCT GAC ATG GGG TGT GTC ATA AAC TGG AAA	2112
Leu Gly Ala Val Val Gln Ala Asp Met Gly Cys Val Ile Asn Trp Lys	
690 695 700	
GGC AAA GAA CTC AAA TGT GGA AGT GGA ATT TTC	2145
Gly Lys Glu Leu Lys Cys Gly Ser Gly Ile Phe	
705 710 715	

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...2175
- (D) OTHER INFORMATION:

180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ATT CTG AAG AGA TGG GGA CAG TTG AAG AAA AAT AAG GCC ATC AGG ATA	48
Ile Leu Lys Arg Trp Gly Gln Leu Lys Lys Asn Lys Ala Ile Arg Ile	
1 5 10 15	
CTG ATT GGA TTC AGG AAG GAG ATA GGC CGC ATG CTG AAC ATC TTG AAC	96
Leu Ile Gly Phe Arg Lys Glu Ile Gly Arg Met Leu Asn Ile Leu Asn	
20 25 30	
GGG AGA AAA AGG TCA ACG ATA ACA TTG CTG TGC TTG ATT CCC ACC GTA	144
Gly Arg Lys Arg Ser Thr Ile Thr Leu Leu Cys Leu Ile Pro Thr Val	
35 40 45	
ATG GCG TTT CAC TTG TCA ACA AGA GAT GGC GAA CCC CTC ATG ATA GTG	192
Met Ala Phe His Leu Ser Thr Arg Asp Gly Glu Pro Leu Met Ile Val	
50 55 60	
GCA AAA CAT GAA AGG GGG AGA CCT CTC TTG TTT AAG ACA ACA GAG GGG	240
Ala Lys His Glu Arg Gly Arg Pro Leu Leu Phe Lys Thr Thr Glu Gly	
65 70 75 80	
ATC AAC AAA TGC ACT CTC ATT GCC ATG GAC TTG GGT GAA ATG TGT GAG	288
Ile Asn Lys Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Met Cys Glu	
85 90 95	
GAC ACT GTC ACG TAT AAA TGC CCC TTA CTG GTC AAT ACC GAA CCT GAA	336
Asp Thr Val Thr Tyr Lys Cys Pro Leu Leu Val Asn Thr Glu Pro Glu	
100 105 110	
GAC ATT GAT TGC TGG TGC AAT CTC ACG TCT ACC TGG GTC ACA TAT GGG	384
Asp Ile Asp Cys Trp Cys Asn Leu Thr Ser Thr Trp Val Thr Tyr Gly	
115 120 125	
ACA TAC ACC CAG AGC GGA GAA CGG AGA CGA GAG AAG CGC TCA GTA GCT	432
Thr Tyr Thr Gln Ser Gly Glu Arg Arg Arg Glu Lys Arg Ser Val Ala	
130 135 140	
TTA ACA CCA CAT TCA GGA ATG GGA TTG GAA ACA AGA GCT GAG ACA TGG	480
Leu Thr Pro His Ser Gly Met Gly Leu Glu Thr Arg Ala Glu Thr Trp	
145 150 155 160	
ATG TCA TCG GAA GGG GCT TGG AAG CAT GCT CAG AGA GTA GAG AGC TGG	528
Met Ser Ser Glu Gly Ala Trp Lys His Ala Gln Arg Val Glu Ser Trp	
165 170 175	
ATA CTC AGA AAC CCA GGA TTC GCG CTC TTG GCA GGA TTT ATG GCT TAT	576
Ile Leu Arg Asn Pro Gly Phe Ala Leu Leu Ala Gly Phe Met Ala Tyr	
180 185 190	
ATG ATT GGG CAA ACA GGA ATC CAG CGA ACT GTC TTC TTT GTC CTA ATG	624
Met Ile Gly Gln Thr Gly Ile Gln Arg Thr Val Phe Phe Val Leu Met	
195 200 205	
ATG CTG GTC GCC CCA TCC TAC GGA ATG CGA TGC GTA GGA GTA GGA AAC	672
Met Leu Val Ala Pro Ser Tyr Gly Met Arg Cys Val Gly Val Gly Asn	
210 215 220	

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AGA GAC TTT GTG GAA GGA GTC TCA GGT GGA GCA TGG GTC GAT CTG GTG Arg Asp Phe Val Glu Gly Val Ser Gly Gly Ala Trp Val Asp Leu Val 225 230 235 240	720
CTA GAA CAT GGA GGA TGC GTC ACA ACC ATG GCC CAG GGA AAA CCA ACC Leu Glu His Gly Gly Cys Val Thr Thr Met Ala Gln Gly Lys Pro Thr 245 250 255	768
TTG GAT TTT GAA CTG ACT AAG ACA ACA GCC AAG GAA GTG GCT CTG TTA Leu Asp Phe Glu Leu Thr Lys Thr Thr Ala Lys Glu Val Ala Leu Leu 260 265 270	816
AGA ACC TAT TGC ATT GAA GCC TCA ATA TCA AAC ATA ACC ACG GCA ACA Arg Thr Tyr Cys Ile Glu Ala Ser Ile Ser Asn Ile Thr Thr Ala Thr 275 280 285	864
AGA TGT CCA ACG CAA GGA GAG CCT TAT CTA AAA GAG GAA CAA GAC CAA Arg Cys Pro Thr Gln Gly Glu Pro Tyr Leu Lys Glu Glu Gln Asp Gln 290 295 300	912
CAG TAC ATT TGC CGG AGA GAT GTG GTA GAC AGA GGG TGG GGC AAT GGC Gln Tyr Ile Cys Arg Arg Asp Val Val Asp Arg Gly Trp Gly Asn Gly 305 310 315 320	960
TGT GGC TTG TTT GGA AAA GGA GGA GTT GTG ACA TGT GCG AAG TTT TCA Cys Gly Leu Phe Gly Lys Gly Gly Val Val Thr Cys Ala Lys Phe Ser 325 330 335	1008
TGT TCG GGG AAG ATA ACA GGC AAT TTG GTC CAA ATT GAG AAC CTT GAA Cys Ser Gly Lys Ile Thr Gly Asn Leu Val Gln Ile Glu Asn Leu Glu 340 345 350	1056
TAC ACA GTG GTT GTA ACA GTC CAC AAT GGA GAC ACC CAT GCA GTA GGA Tyr Thr Val Val Val Thr Val His Asn Gly Asp Thr His Ala Val Gly 355 360 365	1104
AAT GAC ACA TCC AAT CAT GGA GTT ACA GCC ACG ATA ACT CCC AGG TCA Asn Asp Thr Ser Asn His Gly Val Thr Ala Thr Ile Thr Pro Arg Ser 370 375 380	1152
CCA TCG GTG GAA GTC AAA TTG CCG GAC TAT GGA GAA CTA ACA CTC GAT Pro Ser Val Glu Val Lys Leu Pro Asp Tyr Gly Glu Leu Thr Leu Asp 385 390 395 400	1200
TGT GAA CCC AGG TCT GGA ATT GAC TTT AAT GAG ATG ATT CTG ATG AAA Cys Glu Pro Arg Ser Gly Ile Asp Phe Asn Glu Met Ile Leu Met Lys 405 410 415	1248
ATG AAA AAG AAA ACA TGG CTT GTG CAT AAG CAA TGG TTT TTG GAT CTA Met Lys Lys Lys Thr Trp Leu Val His Lys Gln Trp Phe Leu Asp Leu 420 425 430	1296
CCT CTA CCA TGG ACA GCA GGA GCA GAC ACA TCA GAG GTT CAC TGG AAT Pro Leu Pro Trp Thr Ala Gly Ala Asp Thr Ser Glu Val His Trp Asn 435 440 445	1344
TAC AAA GAG AGA ATG GTG ACA TTT AAG GTT CCT CAT GCC AAG AGA CAG Tyr Lys Glu Arg Met Val Thr Phe Lys Val Pro His Ala Lys Arg Gln 450 455 460	1392

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GAT Asp 465	GTG Val	ACA Thr	GTG Val	CTG Leu	GGA Gly 470	TCT Ser	CAG Gln	GAA Glu	GGA Gly 475	GCC Ala 475	ATG Met	CAT His	TCT Ser	GCC Ala 480	CTC Leu 480	1440
GCT Ala	GGA Gly	GCC Ala	ACA Thr	GAA Glu 485	GTG Val	GAC Asp	TCC Ser	GGT Gly	GAT Asp 490	GGA Gly	AAT Asn	CAC His	ATG Met	TTT Phe 495	GCA Ala 495	1488
GGA Gly	CAT His	CTC Leu	AAG Lys 500	TGC Cys	AAA Lys	GTC Val	CGT Arg	ATG Met 505	GAG Glu	AAA Lys	TTG Leu	AGA Arg	ATC Ile 510	AAG Lys	GGA Gly	1536
ATG Met	TCA Ser	TAC Tyr 515	ACG Thr	ATG Met	TGT Cys	TCA Ser	GGA Gly 520	AAG Lys	TTC Phe	TCA Ser	ATT Ile	GAC Asp 525	AAA Lys	GAG Glu	ATG Met	1584
GCA Ala	GAA Glu 530	ACA Thr	CAG Gln	CAT His	GGG Gly 535	ACA Thr 535	ACA Thr	GTG Val	GTG Val	AAA Lys	GTC Val 540	AAG Lys	TAT Tyr	GAA Glu	GGT Gly	1632
GCT Ala 545	GGA Gly	GCT Ala	CCG Pro	TGT Cys	AAA Lys 550	GTC Val	CCC Pro	ATA Ile	GAG Glu	ATA Ile 555	AGA Arg	GAT Asp	GTG Val	AAC Asn	AAG Lys 560	1680
AAA Lys	AAA Lys	GTG Val	GTT Val	GGG Gly 565	CGT Arg	ATC Ile	ATC Ile	TCA Ser	TCC Ser 570	ACC Thr	CCT Pro	TTG Leu	GCT Ala	GAG Glu 575	AAT Asn	1728
ACC Thr	AAC Asn	AGT Ser	GCA Ala 580	ACC Thr	AAC Asn	ATA Ile	GAG Glu	TTA Leu 585	GAA Glu	CCC Pro	CCC Pro	TTT Phe	GGG Gly 590	GAC Asp	AGC Ser	1776
TAC Tyr	ATA Ile	GTG Val 595	ATA Ile	GGT Gly	GTT Val	GGA Gly 600	AAC Asn	AGT Ser	GCA Ala	TTA Leu	ACA Thr	CTC Leu 605	CAT His	TGG Trp	TTC Phe	1824
AGG Arg	AAA Lys 610	GGG Gly	AGT Ser	TCC Ser	ATT Ile	GGC Gly 615	AAG Lys	ATG Met	TTT Phe	GAG Glu	TCC Ser 620	ACA Thr	TAC Tyr	AGA Arg	GGT Gly	1872
GCA Ala 625	AAA Lys	CGA Arg	ATG Met	GCC Ala	ATT Ile 630	CTA Leu	GGT Gly	GAA Glu	ACA Thr	GCT Ala 635	TGG Trp	GAT Asp	TTT Phe	GGT Gly 640	TCC Ser 640	1920
GTT Val	GGT Gly	GGA Gly	CTG Leu	TTC Phe 645	ACA Thr	TCA Ser	TTG Leu	GGA Gly 650	AAG Lys	GCT Ala	GTG Val	CAC His	CAG Gln	GTT Val 655	TTT Phe 655	1968
GGA Gly	AGT Ser	GTG Val	TAT Tyr 660	ACA Thr	ACC Thr	ATG Met	TTT Phe	GGA Gly 665	GGA Gly	GTC Val	TCA Ser	TGG Trp	ATG Met 670	ATT Ile	AGA Arg	2016
ATC Ile	CTA Leu	ATT Ile 675	GGG Gly	TTC Phe	CTA Leu	GTG Val	TTG Leu 680	TGG Trp	ATT Ile	GGC Gly	ACG Thr	AAC Asn	TCA Ser	AGG Arg	AAC Asn	2064
ACT Thr	TCA Ser	ATG Met	GCT Ala	ATG Met	ACG Thr	TGC Cys 695	ATA Ile	GCT Ala	GTT Val	GGA Gly	GGA Gly 700	ATC Ile	ACT Thr	CTG Leu	TTT Phe	2112

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CTG GGC TTC ACA GTT CAA GCA GAG ATG GGT TGT GTG GTG TCA TGG AGT 2160
 Leu Gly Phe Thr Val Gln Ala Glu Met Gly Cys Val Val Ser Trp Ser
 705 710 715 720

GGG AAA GAA TTG AGG 2175
 Gly Lys Glu Leu Arg
 725

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CACTACCGCA AGGTAGAGAG CTCGGCATTC CCTCTTGGTG 40

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GTGATGGCGT TCCATCTCTC GAGCCGTAAC GGAGAACCAC 40

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCCCTGGCGT TCCATCTCTC GAGCCGAGGG GGAGAGCCGC

40

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

ACACTTGCTT TCCACCTCTC GAGCCGAGAT GGAGAGCCGC

40

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GTAATGGCGT TTCACCTCTC GAGCAGAGAT GGCGAACCCC

40

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CCTATCCTTA CTTAAGATCT TCGTGAGTG ACAGAC

36

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(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GGATAGGAAT GAATTCTAGA AGCACCTCAC TGTCTG

36

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CCGCAGAGAT CGTTTTCCTG CCTGCATGAT TCC

33

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

CCGATCCTAA TTTAAGATCT TTGTGCAGGG AAAGCC

36

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CCTATCCCAA CTTGAGATCT TTATGAAGAT ACAGTA

36

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CCTAACCGTG CTTGAGATCT TTGTGAAGTT ACCGAC

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WHAT IS CLAIMED IS:

1. A quadravalent vaccine providing immunity against all four serotypes of dengue virus comprising a DEN-2 PDK-53 infectious clone-derived virus.

5 2. A quadravalent vaccine providing immunity against all four serotypes of dengue virus comprising a chimeric DEN-2/1 virus.

3. A quadravalent vaccine providing immunity against all four serotypes of dengue virus comprising a
10 chimeric DEN-2/3 virus.

4. A quadravalent vaccine providing immunity against all four serotypes of dengue virus comprising a chimeric DEN-2/4 virus.

5. A quadravalent vaccine providing immunity
15 against all four serotypes of dengue virus comprising DEN-2 PDK-53 infectious clone-derived and chimeric DEN-2/1, DEN-2/3, and DEN-2/4 viruses.

6. A method of immunization in which a desired
immune response is produced against all four serotypes of
20 dengue virus comprising the step of administering to a subject a quadravalent vaccine comprising DEN-2 PDK-53 infectious clone-derived and chimeric DEN-2/1, DEN-2/3, and DEN-2/4 viruses.

7. A composition of matter comprising a full
25 genome-length infectious cDNA clone for a DEN-2 virus, strain 16681.

8. A composition of matter comprising a full genome-length infectious cDNA clone for a DEN-2 virus of a

strain characterized as replicating to high titer in cell culture.

9. A composition of matter comprising a full genome-length infectious cDNA clone for a DEN-2 virus, strain 16681, having the identifying characteristics of ATCC 69826.

10. A composition of matter comprising a full genome-length infectious cDNA clone for a DEN-2 virus, strain 16681, attenuated derivative, PDK-53.

10 11. A composition of matter comprising a full genome-length infectious cDNA clone for a DEN-2 virus attenuated derivative, characterized as replicating to high titer in cell culture.

15 12. A composition of matter comprising a full genome-length infectious cDNA clone for a DEN-2 virus, strain 16681, attenuated derivative, PDK-53, having the identifying characteristics of ATCC 69825.

20 13. A composition of matter comprising a full genome-length infectious cDNA clone of a chimeric DEN-2/1 virus, wherein said virus is characterized as the expressing prM and E genes of a DEN-1 attenuated virus in the context of the nonstructural genes of the DEN-2 PDK-53 virus.

25 14. The composition of matter of Claim 13, wherein said DEN-1 attenuated virus is DEN-1 PDK-13.

15. A composition of matter comprising a full genome-length infectious cDNA clone of a chimeric DEN-2 virus, wherein said virus is characterized as expressing the antigenicity of a DEN-1 attenuated virus.

16. A composition of matter comprising a full genome-length infectious cDNA clone of a chimeric DEN-2/3 virus, wherein said virus is characterized as expressing the prM and E genes of a DEN-3 attenuated virus in the context of the nonstructural genes of the DEN-2 PDK-53 virus.

17. The composition of matter of Claim 16, wherein said DEN-3 attenuated virus is DEN-3 PGMK30/FRhL-3.

18. A composition of matter comprising a full genome-length infectious cDNA clone of a chimeric DEN-2 virus, wherein said virus is characterized as expressing the antigenicity of a DEN-3 attenuated virus.

19. A composition of matter comprising a full genome-length infectious cDNA clone of a chimeric DEN-2/4 virus, wherein said virus is characterized as expressing the prM and E genes of a DEN-4 attenuated virus in the context of the nonstructural genes of the DEN-2 PDK-53 virus.

20. The composition of matter of Claim 19, wherein said DEN-4 attenuated virus is DEN-4 PDK-48.

21. A composition of matter comprising a full genome-length infectious cDNA clone of a chimeric DEN-2 virus, wherein said virus is characterized as expressing the antigenicity of a DEN-4 attenuated virus.

22. A genetic construct comprising a DNA sequence operably encoding the polyprotein of DEN-2 virus, strain 16681.

23. The genetic construct of Claim 22, wherein said polyprotein is the polyprotein encoded by the nucleotide sequence of SEQ ID NO:1.

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24. A genetic construct comprising a DNA sequence operably encoding at least one protein of DEN-2 virus, strain 16681.

5 25. The genetic construct of Claim 24, wherein said protein is a protein encoded by the nucleotide sequence of SEQ ID NO: 1.

26. A genetic construct comprising a DNA sequence operably encoding the polyprotein of DEN-2 virus, strain 16681, attenuated derivative, PDK-53.

10 27. The genetic construct of Claim 26, wherein said polyprotein is the polyprotein encoded by the nucleotide sequence of SEQ ID NO:2.

15 28. A genetic construct comprising a DNA sequence operably encoding at least one protein of DEN-2 virus, strain 16681, attenuated derivative, PDK-53.

29. The genetic construct of Claim 28, wherein said protein is a protein encoded by the nucleotide sequence of SEQ ID NO: 2.

20 30. A genetic construct comprising a DNA sequence operably encoding at least one structural protein of DEN-1 PDK-13.

31. The genetic construct of Claim 30, wherein said structural protein is a structural protein encoded by the nucleotide sequence of SEQ ID NO: 124.

25 32. A genetic construct comprising a DNA sequence operably encoding at least one structural protein of DEN-3 PGMK30/FRhL-3.

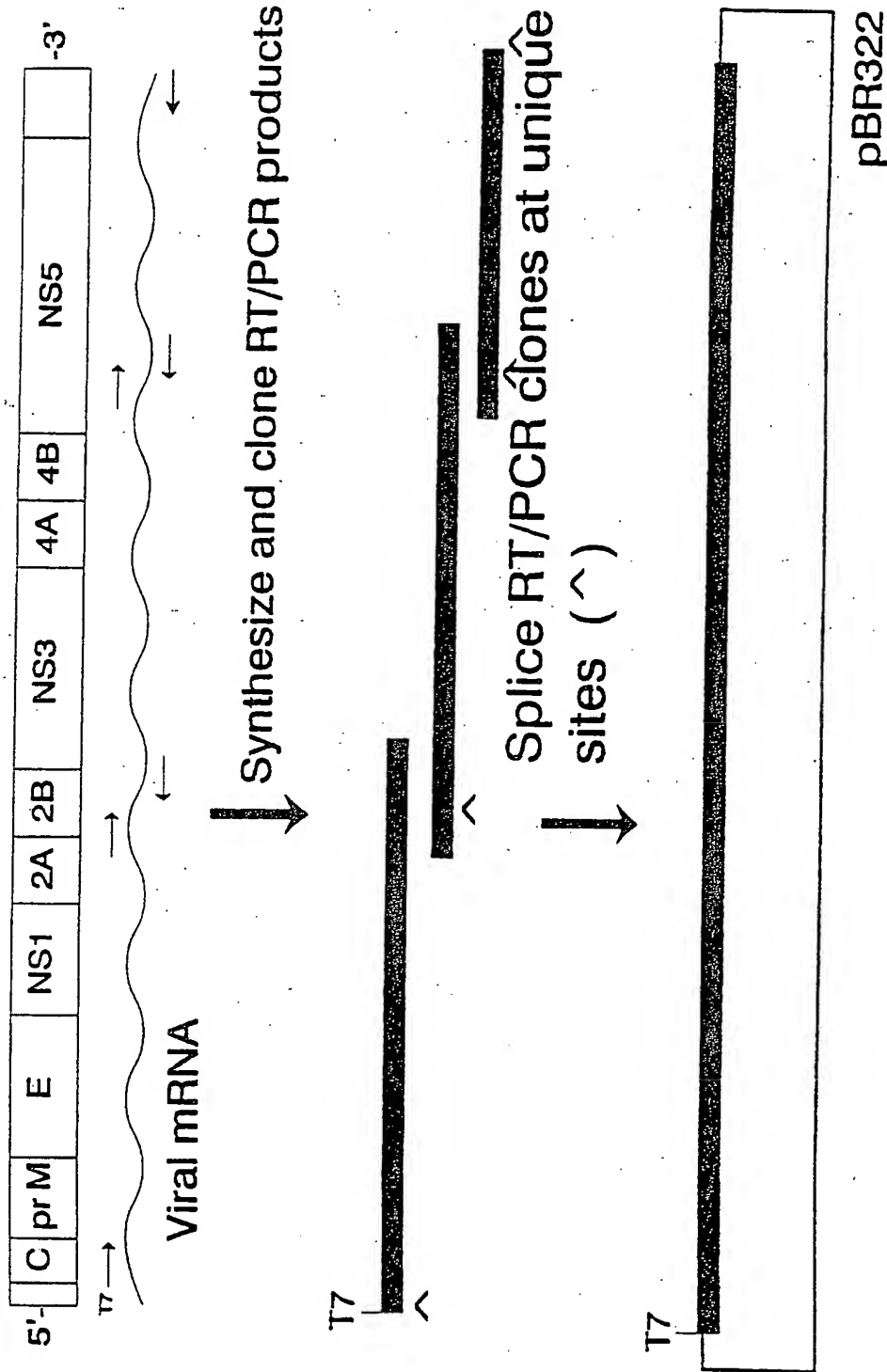
30 33. The genetic construct of Claim 32, wherein said structural protein is a structural protein encoded by the nucleotide sequence of SEQ ID NO: 125.

34. A genetic construct comprising a DNA sequence operably encoding at least one structural protein of DEN-4 PDK-48.

35. The genetic construct of Claim 34, wherein said
5 structural protein is a structural protein encoded by the nucleotide sequence of SEQ ID NO: 126.

36. A host cell comprising the genetic construct of any of Claims 22-35.

Construction of DEN-2 Infectious cDNA Clone



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FIGURE 1

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Transcription of DEN-2 RNA from Infectious Clone

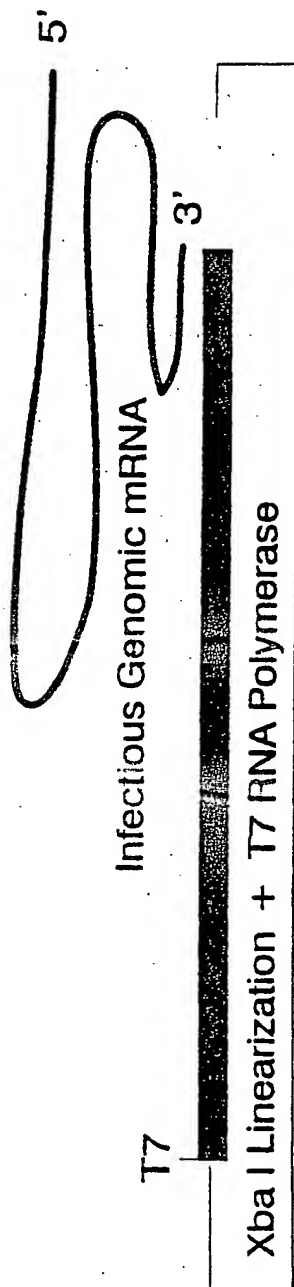
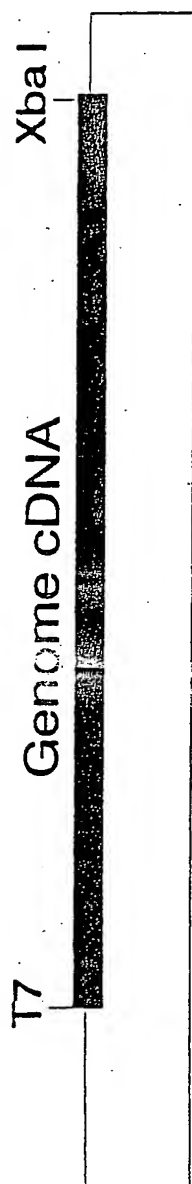
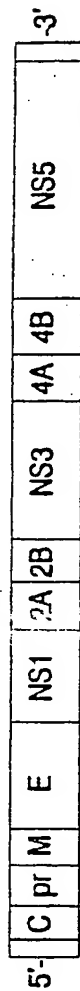


FIGURE 2

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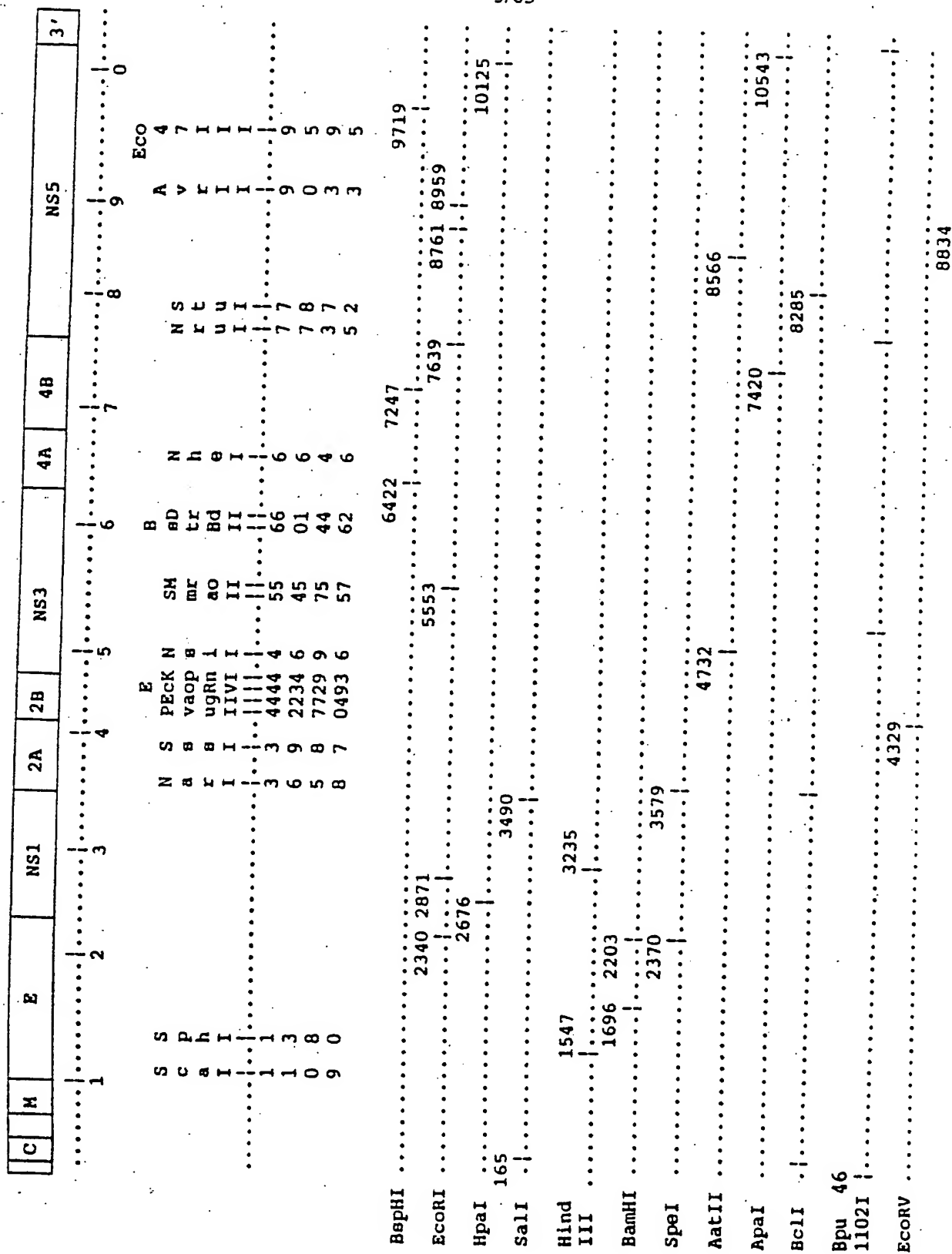


FIGURE 3A

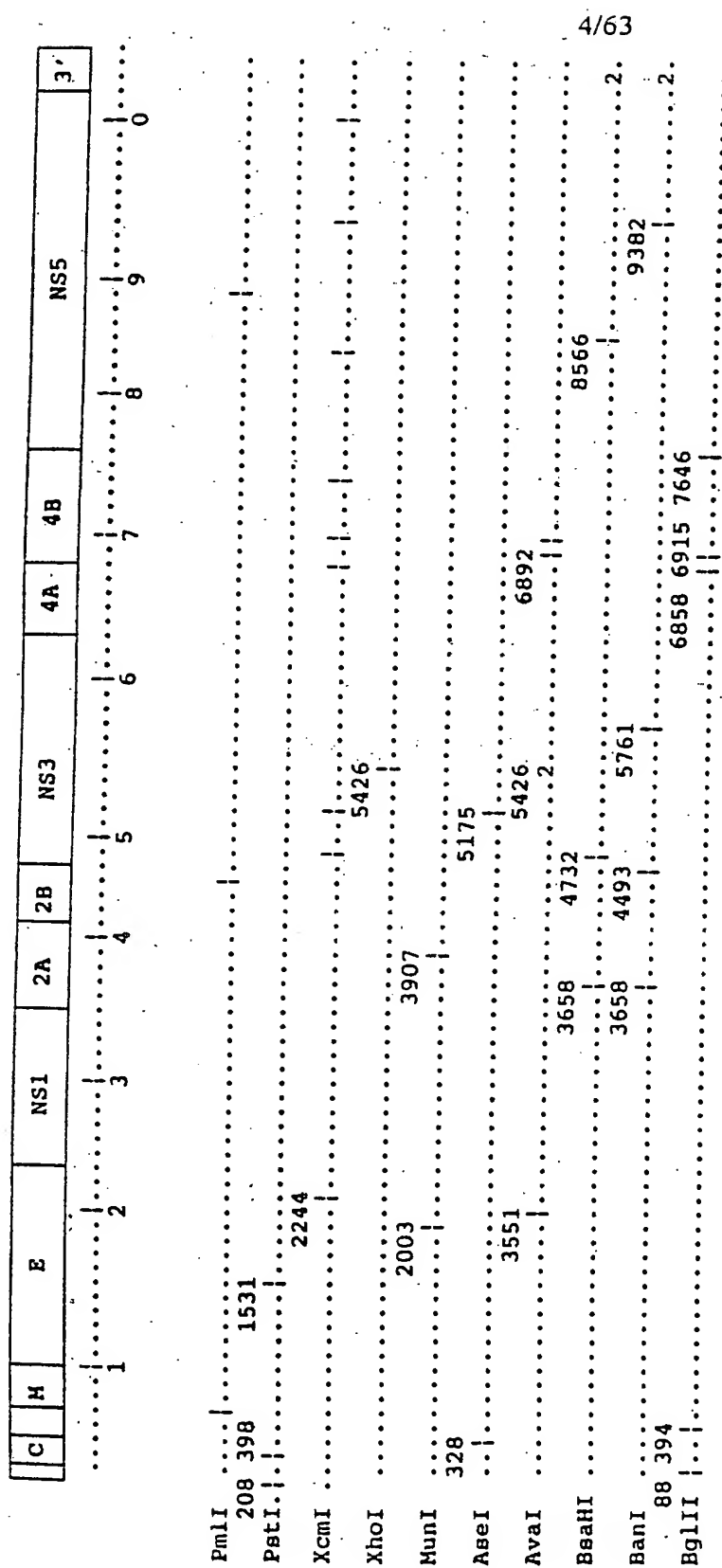
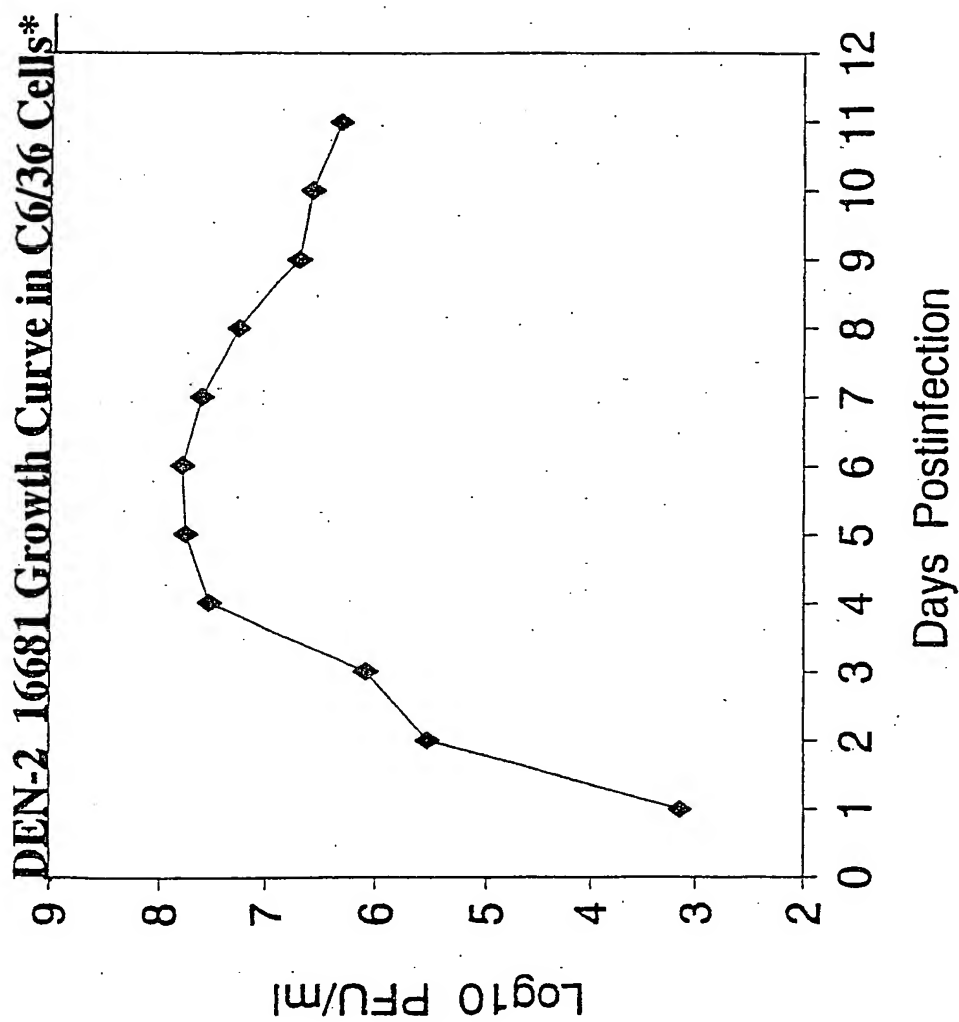


FIGURE 3B

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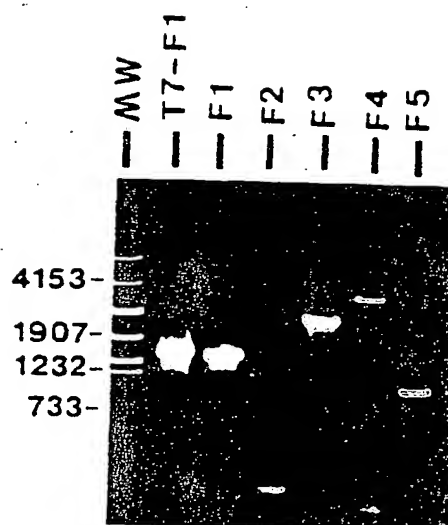


* M.O.I. = 0.004, 150cm², 40 ml

FIGURE 4

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FIGURE 5A



HMC

FIGURE 5B

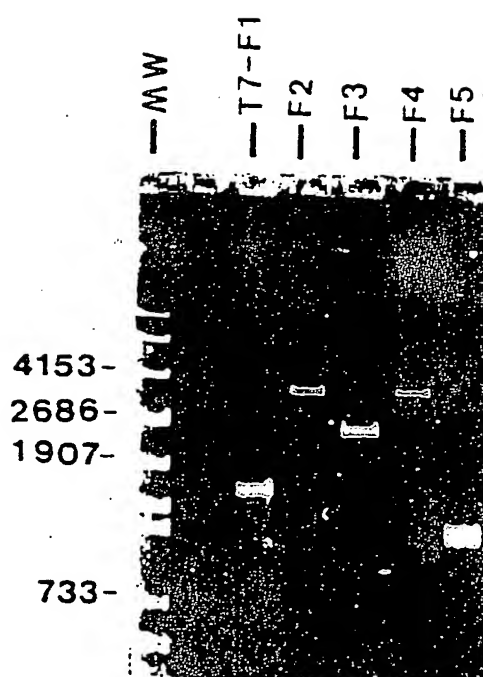
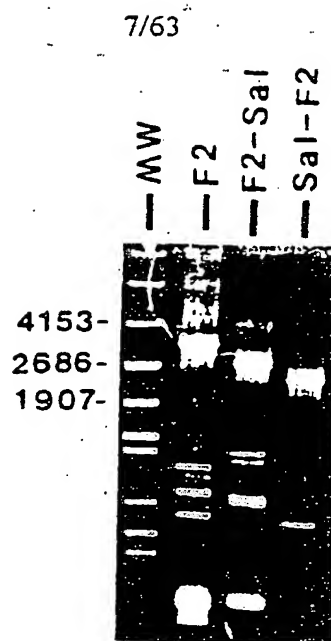
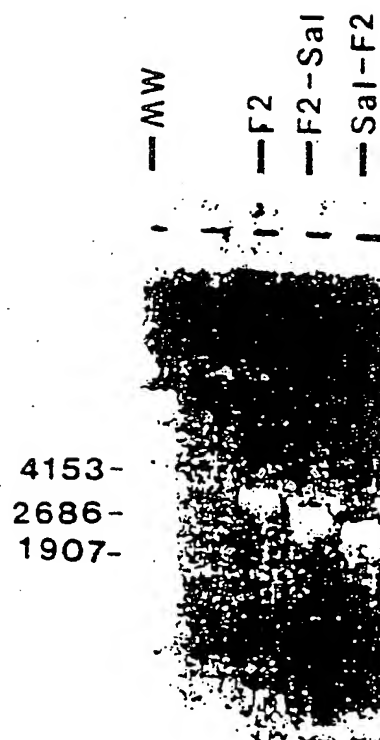


FIGURE 5C



HMC

FIGURE 5D



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B	RT/PCR Amplicon	Expected Amplicon Length	Up-Amplimer	Down-Amplimer
	T7-F1	1552-bp	D2-SMT71	cD2-1503
	F2	3327-bp	D2-1261	cD2-4557
	F2-Sal	2742-bp	D2-1261	cD2-4002
	Sal-F2	2388-bp	D2-2170	cD2-4557
	F3	2368-bp	D2-4257	cD2-6624
	F4	3304-bp	D2-6493	cD2-9796
	F5	1032-bp	D2-9656	cD2-10687.Xba

FIGURE 5E

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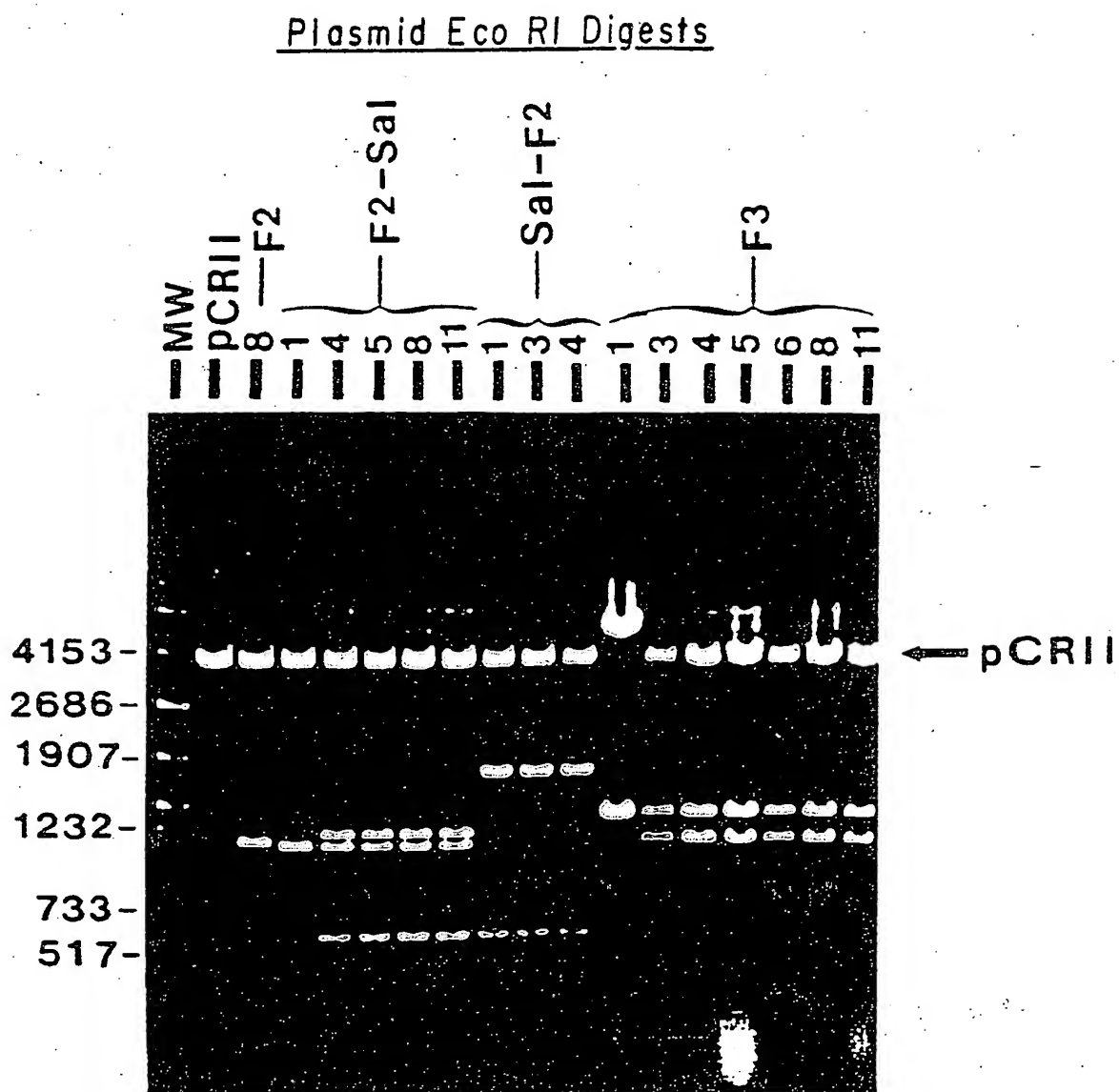


FIGURE 6

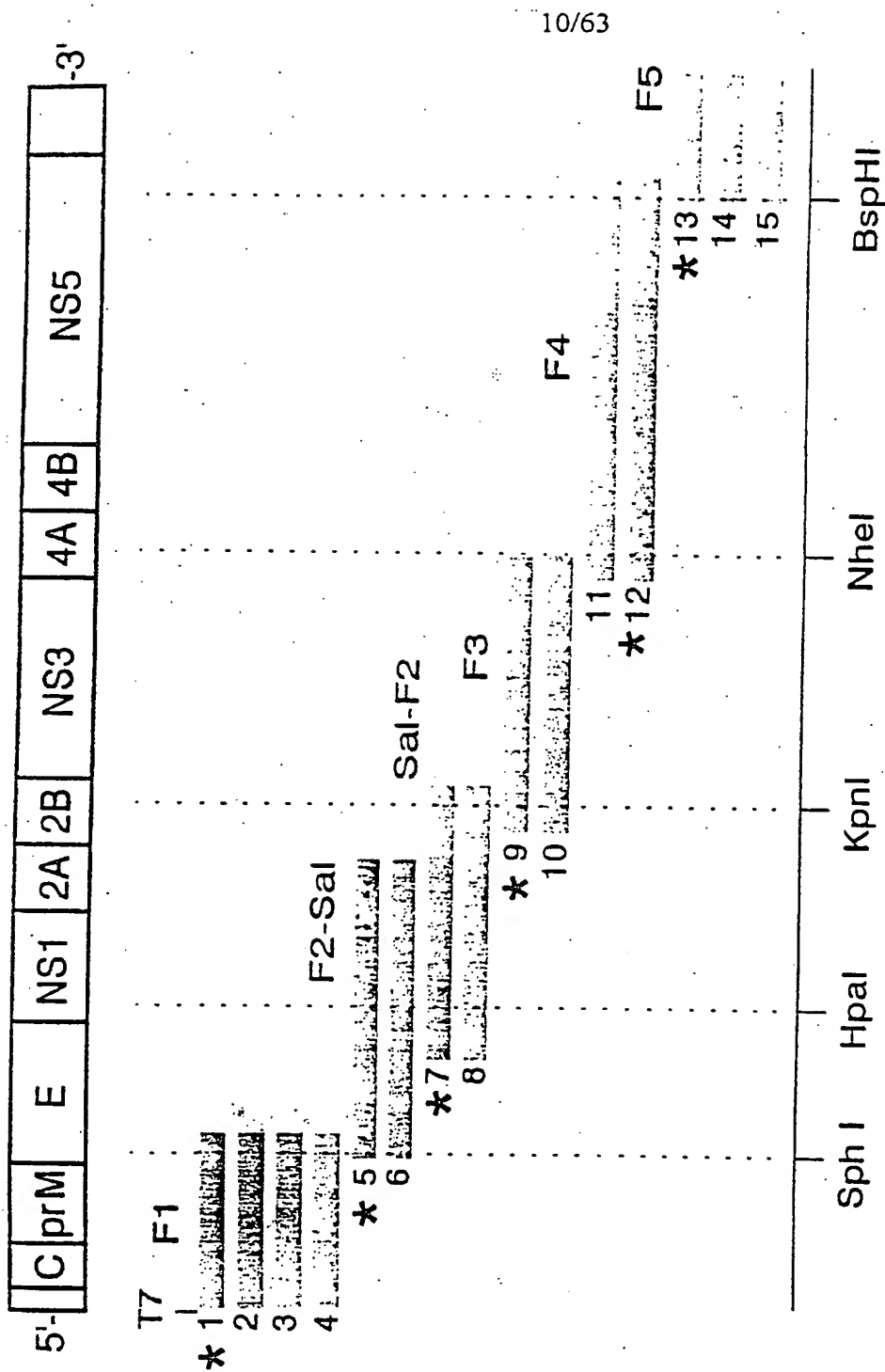


FIGURE 7

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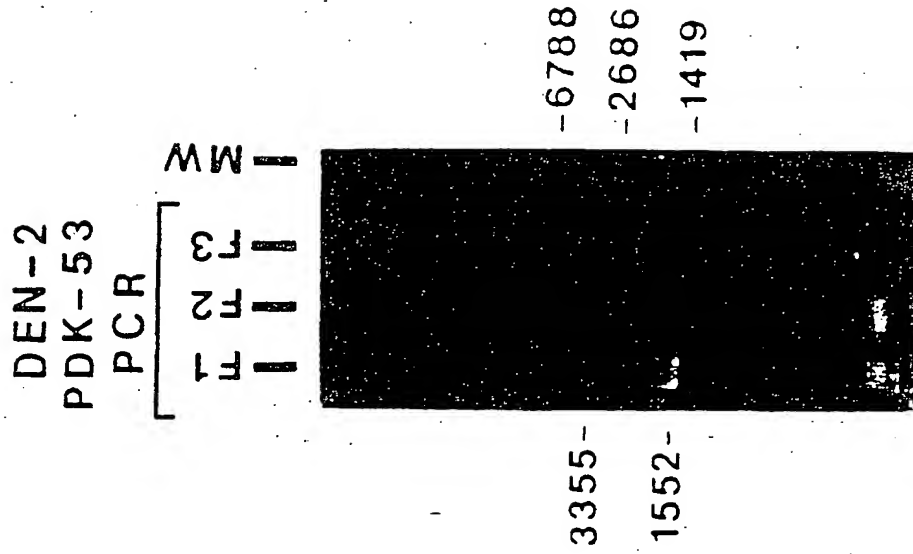


FIGURE 8B

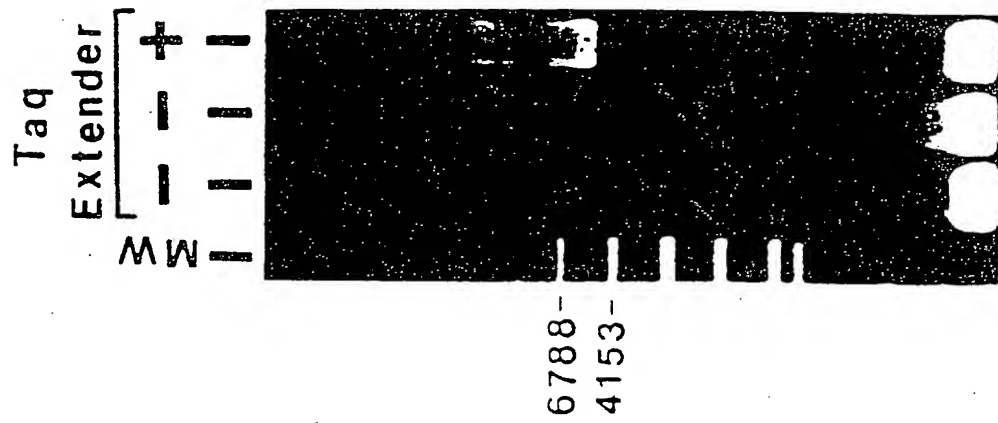
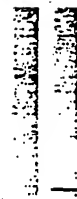


FIGURE 8A

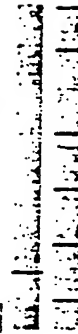
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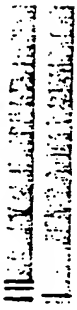
T7 F1



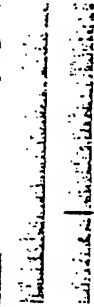
F2-Sal



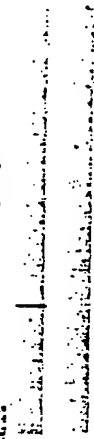
Sal-F2



F3

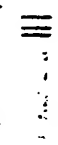
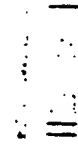


F4



F5

... = cDNA Clone "Error"



Sph I Hpa I Kpn I Nhe I Bsp HI

FIGURE 9

13763

C	H	E	NS1	2A	2B	NS3	4A	4B	NS5	3'NC
▲	▲		▲	▲▲▲	▲▲	▲	▲	▲▲▲▲	▲	▲▲
▲	▲			▲▲	▲	▲		▲▲▲	▲	▲▲
▲	▲			▲▲	▲	▲	▲	▲	▲	▲▲
▲				▲▲	▲					▲▲
▲				▲▲	▲					▲▲
▲				▲▲	▲					▲

FIGURE 10

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	<u>5'-NC</u>	<u>Capsid</u>	<u>PrM</u>	<u>E</u>	<u>NS1</u>	<u>NS2A</u>
		1 1 2 2 2 3	6 7	1	3	3 3 3 3 3 3 3 3
	4 6 7	0 3 1 2 3 2	5 0	4	0	6 6 7 8 8 8 8 9
	9 9 7	3 2 0 6 6 1	1 3	5	1	1 4 7 0 0 2 2 8
DEN-2-16681.RK	A A A	A T G T T A	G G	T	T	C G A C T C T A
DEN-2-16681.BLOK	G T G	G A A C A C	C C	C	C	T A C T C T C G
		■ ■ ■ ■ ■ ■	■ ■ ■ ■ ■ ■	■ ■ ■ ■ ■ ■	■ ■ ■ ■ ■ ■	■ ■ ■ ■ ■ ■
	<u>NS2A</u>	<u>NS2B</u>	<u>NS3</u>	<u>NS4A</u>	<u>NS4B</u>	
	4 4 4	4 4	5 5 5 5 5 6 6	6	6 6 7 7 7 7 7	
	0 0 0	2 3	0 0 6 7 9 1 1	5	8 8 1 1 2 4 5	
	1 4 6	4 4	3 7 4 0 5 1 1	8	6 7 3 9 1 0 6	
	8 4 2	1 4	4 6 9 5 5 3 4	0	4 0 9 6 3 3 1	
DEN-2-16681.RK	C A A	T T	C G G T T A A	T	C G T G A C A	
DEN-2-16681.BLOK	T G G	C C	T A C C C C C	C	A A C C T T G	
	■ ■ ■	■ ■	■ ■ ■ ■ ■ ■ ■	■ ■	■ ■ ■ ■ ■ ■ ■	
	<u>NS5</u>	<u>3'-NC</u>				
	8 8 9 9 9 9 9 9 9 9	1 1 1 1 1 1 1 1				
	5 9 2 2 3 5 5 6 6 7 8	0 0 0 0 0 0 0 0				
	4 3 0 2 0 9 9 2 2 3 4	3 6 6 6 6 6 6 6				
	2 1 7 1 3 1 2 0 1 2 5	3 3 4 5 5 5 5 7				
		0 7 6 1 2 5 9 3				
DEN-2-16681.RK	G G C A G C G T G T C	G A G T G G C C				
DEN-2-16681.BLOK	T C T C C G C C A C A	C C A A A A A T				
	■ ■ ■ ■ ■ ■ ■ ■	■ ■ ■ ■ ■ ■ ■ ■				

FIGURE 11

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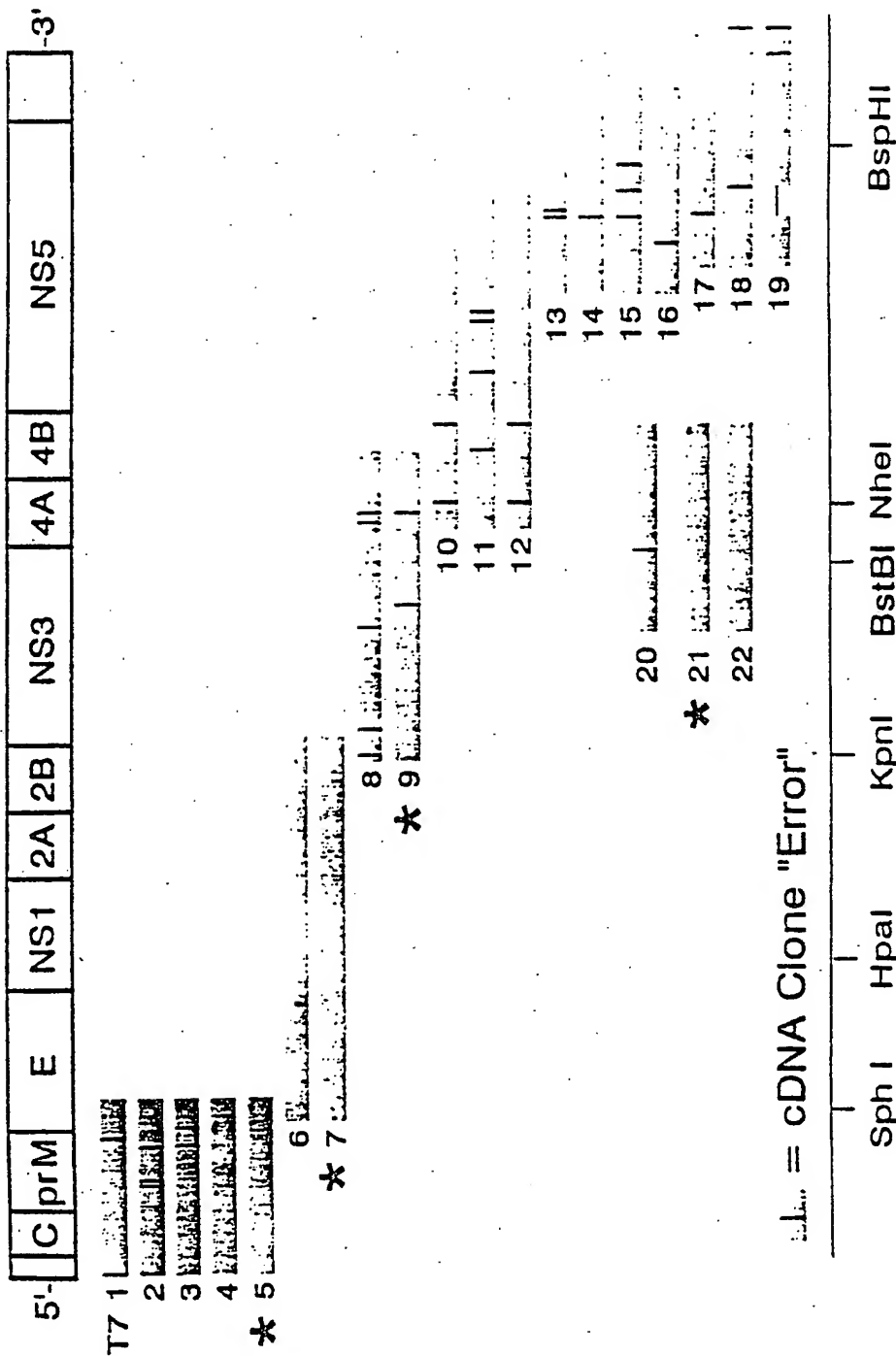


FIGURE 12

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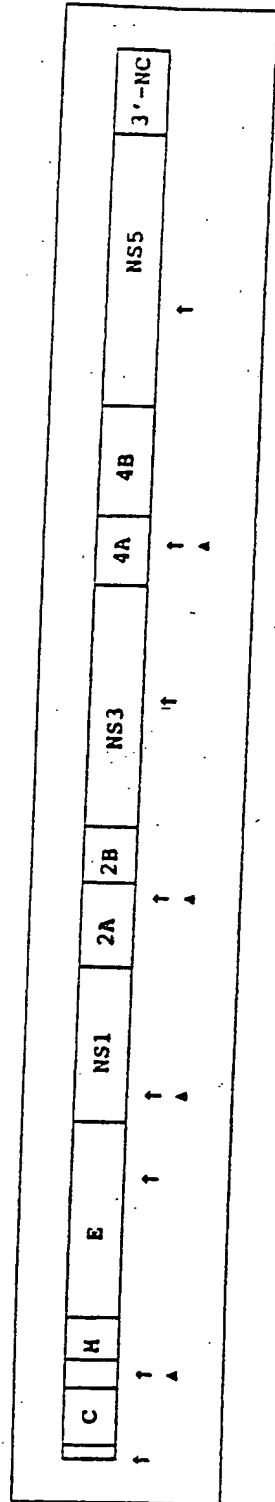


FIGURE 13

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Amplimer D2-SHT71 - **ECORI** **MluI** **T7 Promoter**
SetI

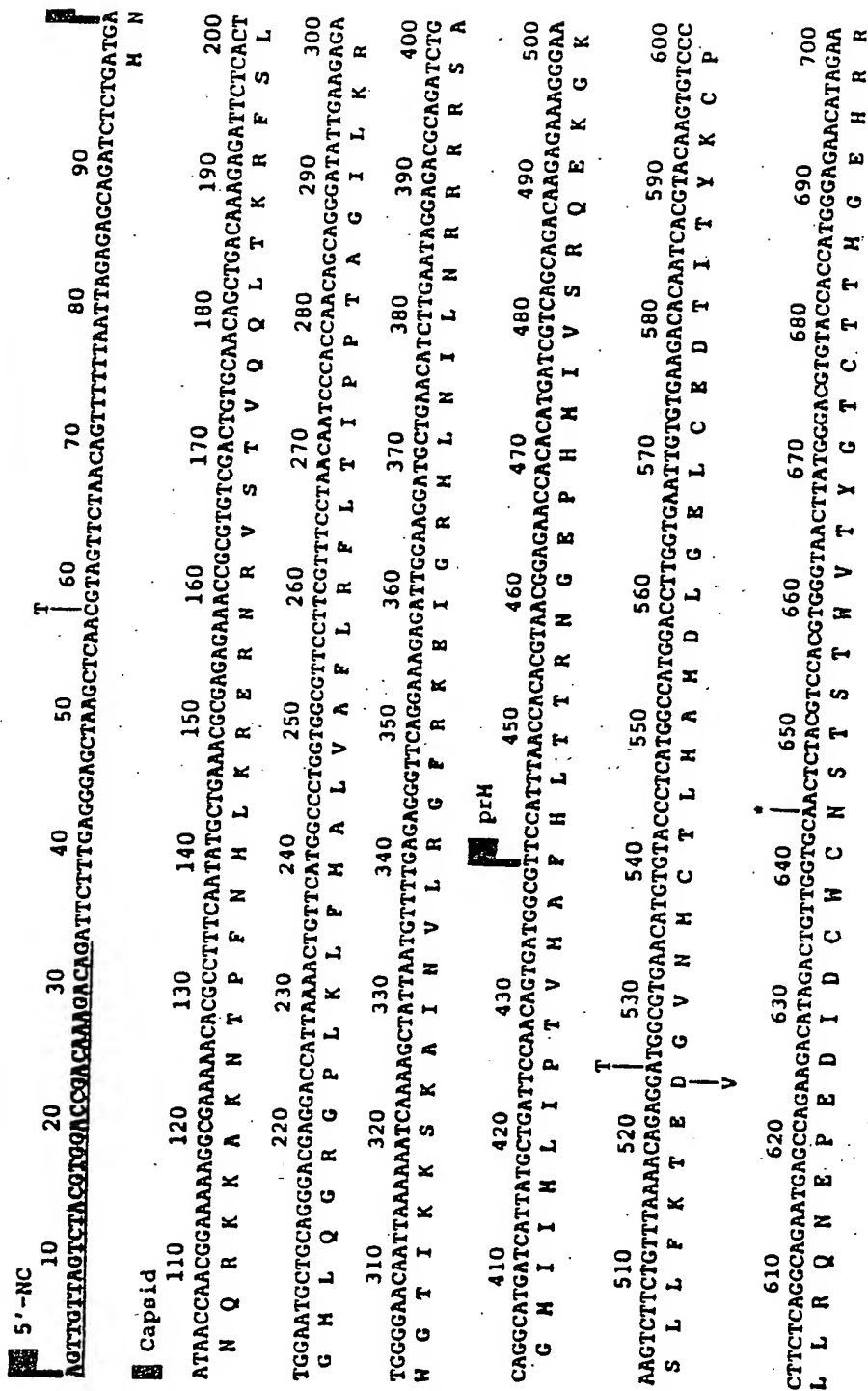


FIGURE 14A

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710 M 720 730 740 750 760 770 780 790 800
 GAGAAAGATCAGTGGCACTGGTCCACATGTGGGAAATGGGACTGGACACAGCACTGAACATGCTATCATCAGAGGGGCTTGGAAACATGTCCA
 E K R S V A L V P H V G H G L E T R T E T W H S S E G A W K H V Q
 810 820 830 840 850 860 870 880 890 900
 GAGAAATGAACTTGGATCTTGAGACATCCAGGCTTCACCATGATGGCAGCAATCTGGCATACACCATAGGAACGACACATTTCCAAAGAGCCCTGATT
 R I E T W I L R H P G F T M H A A I L A Y T I G T T H F Q R A L I
 910 920 930 940 950 960 970 980 990 1000
 TTCATCTTACTGACAGCTGTCACTCTTCAATGACAAATGCTTGCATGAGAAATGTCAATAGAGACTTTGTGAGGGGTTTCAGGAGGAGGCTGGGTTG
 F I L L T A V T P S M T H R C I G H S N R D F V E G V S G G S W V D
 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100
 ACATAGTCTTAGAATGGAGCTGTGACACAGGATGGCAAAACAAACCAACATTTGGAATGATAAACAAGAGCCAAACAGCCTGCCAC
 I V L E H G S C V T T H A K N K P T L D F E L I K T E A K Q P A T
 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
 CCTAAGGAAGTACTGTATAGAGGCAAGCTTAACCAACACACAGAACTTGGTCCCAACACAGGGGACCCAGCCTAAATGAAGACAGGACACAA
 L R K Y C I E A K L T N T T T E S R C P T Q G E P S L N E E Q D K
 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
 AGTTTCCTCTGCAAAACACTCCATGGTAGACAGGATGGGGAATGGATGTGGACTATTGGAAAGGGAGGCAATGTGACCTGTGCTATGTTTCAGATGCA
 R F V C K H S M V D R G W G N G C G L F G K G G I V T C A H F R C K
 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400
 AAAGAACATGGAGGAAAGTTGTGCACAGAGAACTTGGAAATACACCATTTGTGATACACCTCACTCAGGGGAGAGCATGCAGTCGGAATGACAC
 K N H E G K V V Q P E N L E Y T I V I T P H S G E E H A V G N D T
 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500
 AGGAAACATGGCAGGAATCAAAATACACACAGAGTCCATCAGAGAGCAAGAAATGACAGGTTATGGCACTGTCAATGAGAGTCTCTCCACGA
 G K H G K E I K I T P Q S S I T E A E L T G Y G T V T H E C S P R
 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600
 ACGGCGCTCGACTTCAATGATGGTGTGCTGCAGATGGAAATGAAGCTTGGCTGGTCCAGAGCCAAATGTTCTTACAGCCTGCCGTTACCATGGTTGC
 T G L D F N E H V L L Q M E N K A W L V H R Q W F L D L P L P W L P

SphI

FIGURE 14B

1510 1620 1630 1640 1650 1660 1670 1680 1690 1700
 CCGAGCGGACACACAGAGGTCAATTCGATACAGAAAGACATGGTGCACCTTCAAAAATCCCATCGGAAGAACGAGTGTGTTGTTTAGGATC
 G A D T Q G S N H I Q K E T L V T F K N P H A K K Q D V V V L G S

1710 1720 1730 1740 1750 1760 1770 1780 1790 1800
 CCAAGAGGGGCCATGCACACAGCACCTACAGGGGCCACAGAAATCCAAATGTCATCAGGAACTTACTTTCACAGGACATCTCAAGTGCAGGCTGAGA
 Q E G A H H T A L T G A T B E I Q H S S G N L L F T G H L K C R L R

1810 1820 1830 1840 1850 1860 1870 1880 1890 1900
 ATGGACAGCTACAGCTCAAGGAATGTCATACTCTATGTGCACAGGAAAGTTAAAGTTGTGAAGGAATAGCAGAAACACACATCGGAACAAATAGTTA
 M D K L Q L K G H S Y S H C T G K F K V V K E I A E T Q H G T I V I

1910 1920 1930 1940 1950 1960 1970 1980 1990 2000
 TCAGAGTGCNAATAGAGGGACGGCTCCATGCAGATCCCTTTGAGATAATGGAATGGAAAGACATGTCTTAGTGCCTGATTACAGTCAA
 R V Q Y E G D G S P C K I P F E I M D L E K R H V L G R L I T V N

2010 2020 2030 2040 2050 2060 2070 2080 2090 2100
 CCCAATTGTGACAGAAAGATAGCCCGTCAACATAGAGGACAGAACCTCCATTCGGAGACAGCTACATCATAGGAGTAGACGCGGACAACTGAAG
 P I V T E K D S P V N I E A E P P F G D S Y I I I G V E P G Q L K

2110 2120 2130 2140 2150 2160 2170 2180 2190 2200
 CTCACACTGGTTAAGAAAGAAAGTTCTATCGGCCCAATGTTTCAGACACACATGAGGGGGGGAAGAGAAATGGCCATTTTAGGTGACACAGCTGGGATT
 L N W F K K G S S I G Q H F E T T H R G A K R H A I L G D T A W D F

2210 2220 2230 2240 2250 2260 2270 2280 2290 2300
 TTGGATCCTTGGAGGAGTCTTACATCTATAGGAAGGCTCTCCACCAAGTCTTTGGAGCAATCTATGGAGCTGCCTTCAGTGGGTTTCATGGACTAT
 G S L G G V F T S I G K A L H Q V F G A I Y G A A F S G V S W T H

2310 2320 2330 2340 2350 2360 2370 2380 2390 2400
 GAAATCCTATAGGAGTCAATATACATGATAGGAATGAATTCACGACCACTACTGTCTGTGACACTAGTATTGTGGGAATTTGACACACTGTAT
 K I L I G V I I T W I G H N S R S T S L S V T L V L V G I V T L Y

2410 2420 2430 2440 2450 2460 2470 2480 2490 2500
 TTGGGAGTCAATGGTGCAGCCGATAGTGGTTGCTGTGAGCTGGAAACAAAGAACTGAATGTGGCAGTGGGATTTTCATCAGACAAACGTCGACA
 L G V H V Q A D S G C V V S W K N K E L K C G S G I F I T D N V H T

FIGURE 14C

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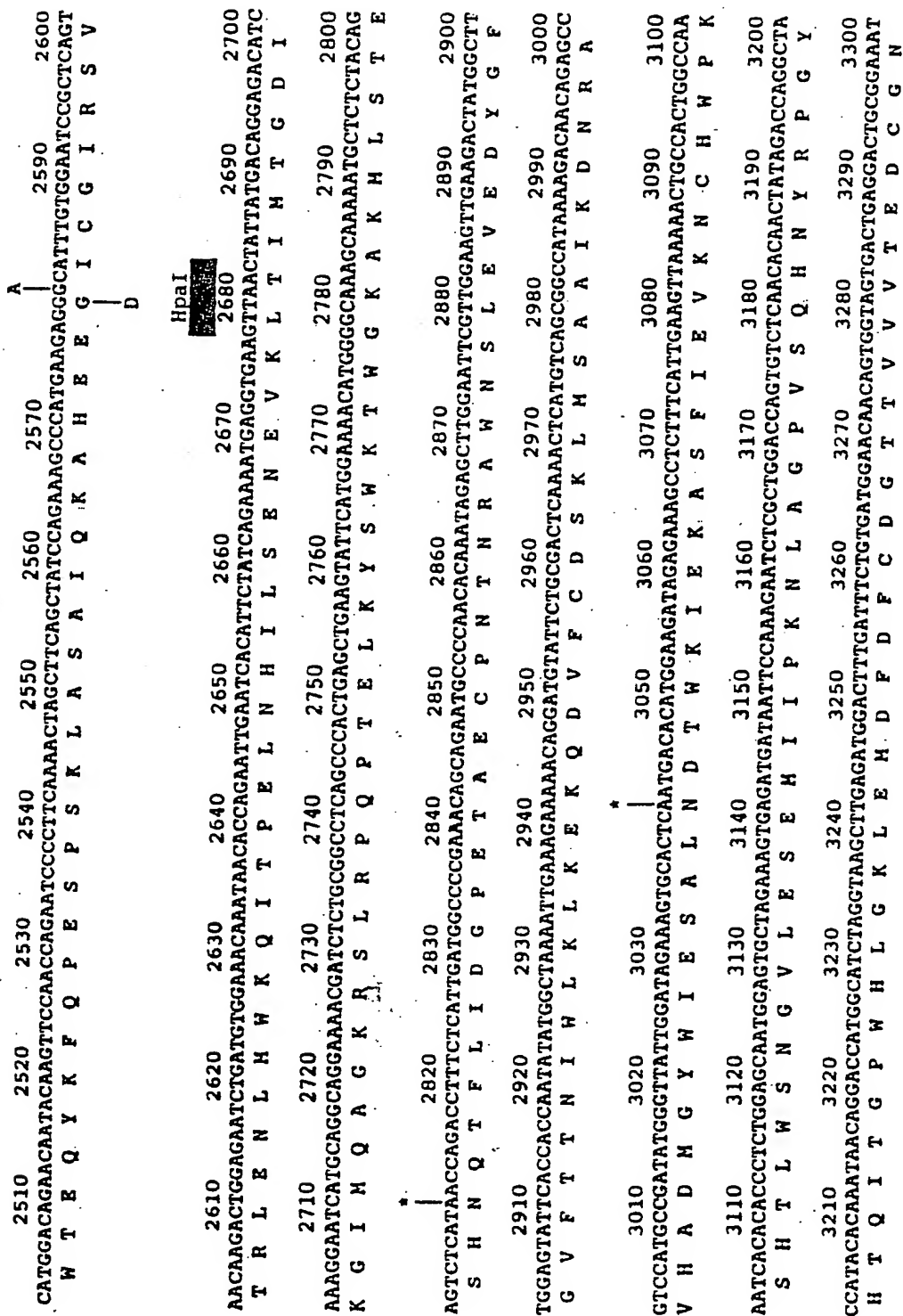


FIGURE 14D

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3310 3320 3330 3340 3350 3360 3370 3380 3390 3400
 AGAGGACCCCTTTGAGAACACACCTGCTCTGGAACATCATACAGAAATGGTGTGCGCATCTTGACACATTACACCGCTAAGATACAGAGGTGAGG
 R G P S L R T T A S G K L I T E W C C R S C T L P P L R Y R G E D
 3410 3420 3430 3440 3450 3460 3470 3480 3490 3500
 ATGGGTGCTGTACGGGATGGMAANTCAGACCATTTGAGGAGAAAGAGAGAAATTTGGTCAACTCCTTGGTCACAGCTGGACATGGCAGTGGCAACTT
 G C H Y G H E I R P L K E K E E N L V N S L V T A G H G Q V D N F
 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600
 TTCACAGGAGCTTGGGANTGGCATTTCTTGGAGGAATGCTTAGGACCCGAGTAGGACCAACATGCAATACACTAGTTGACAGTTCTTTTGTG
 S L G V L G H A L F L E E H L R T R V G T K H A I L L V A V S F V
 3610 3620 3630 3640 3650 3660 3670 3680 3690 3700
 ACATTGATCAGGGAAACATGTCCTTTAGAGACCTGGGAGAGCTGATGGTTATGGTAGGCGCACTATGACGGATGACATAGGTATGGCGTACTATC
 T L I T G N H S F R D L G R V H V H V G A T H T D D I G H G V T Y L
 3710 3720 3730 3740 3750 3760 3770 3780 3790 3800
 TTGCCCTACTAGCAGCCTTCANAGTCAGACCAACTTTTGGAGCTGGACTACTCTTGAGAAAGCTGACCTCCAGGAAATGATGACTACTATAGGAAT
 A L L A A F K V R P T F A A G L L L R K L T S K E L H M T T I G I
 3810 3820 3830 3840 3850 3860 3870 3880 3890 3900
 TGTACTCTCTCCAGAGCACCATACAGACCATTTCTTGGATGACTGATGCGTTAGCCTTAGCATGATGTCCTCMAAATGGTGAGAAATATGGAA
 V L L S Q S T I P E T I L E L T D A L A L G H M V L K H V R N H E
 3910 3920 3930 3940 3950 3960 3970 3980 3990 4000
 AAGTATCAATTTGGCAGTGACTATCATGCTATCTTGTGCTCCCAAGCAGTGATATTACAAACGCATGGAAAGTGAGTTGCACAAATATGGCAGTGG
 K Y Q L A V T I H A I L C V P N A V I L Q N A W K V S C T I L A V V
 4010 4020 4030 4040 4050 4060 4070 4080 4090 4100
 TGTCGTTTCCCACTGCTCTTAACATCCTCACAGCAAAACAGATTTGGATACCATTTGACATGCGATCAAAAGGTCTCAATCCACAGCTATTTTCT
 S V S P L L L T S S Q Q K T D W I P L A L T I K G L N P T A I F L
 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200
 AACACCCCTCTCAAGACCAAGCAAGAAAGGAGCTGGCCATTAATGAGGCTATCATGCGAGTGGGATGGTGAGCAATTTAGCCAGTTCTCTCTCTAA
 T T L S R T S K K R S W P L N E A I H A V G H V S I L A S S L L K

FIGURE 14E

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4210 4220 4230 4240 4250 4260 4270 4280 4290 4300
 AATGATATCCNTGACAGGACCATTTAGTGGCTGGAGGGCTCCTCACTGTGCTACGTGCTCACTGGACCATGGCCGANTTGGAACTGGAGAGAGCAG
 N D I P H T G P L V A G G L L T V C Y V L T G R S A D L E L E R A A
 4310 4320 4330 4340 4350 4360 4370 4380 4390 4400
 CCGATGTCAATGGAGACCCAGGAGAGATATCAGGAGCACTCCATCCCTGTCAATCAATATCAGAAGATGGTAGCATGTGATATAAAATGAAGA
 D V K H E D Q A E I S G S S P I L S I T I S E D G S H S I K N E E
 4410 4420 4430 4440 4450 4460 4470 4480 4490 4500
 GGAAGAACAACTGACCATCTACTATTAGAACAGGATTGCTGGTATCTCAGGACTTTTCTCTGTATCAATACCAATCAACGAGCAGCATGTACCTG
 E E Q T L T I L I R T G L L V I S G L F P V S I P I T A A A W Y L
 4510 4520 4530 4540 4550 4560 4570 4580 4590 4600
 TGGGAAGTGAAGAACACGCGGAGTATTCGGGATGTTCTTCCACCCCAACCCATGGAAAGGCTGAACCTGGAAGATGGAGCCTATAGCAATTAAGC
 W E V K K Q R A G V L W D V P S P P P H G K A E L E D G A Y R I K Q
 4610 4620 4630 4640 4650 4660 4670 4680 4690 4700
 AAAAGGATTTCTGCATATCCAGATCGGAGCCGGAGTTACAAAGAGGAACATCCATACATGTGGCATGTGCACACCTGGCGCTGTCTAATGCA
 K G I L G Y S Q I G A G V Y K E G T F H T H W H V T R G A V L M H
 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800
 TAAGGAAGAGGATTGAACCATCATGCGGACGACGTCAAGAAAGACCTAATATCATATGGAGGAGGCTGGAGTTAGAGAGCAATGGAGAGGAGAA
 K G K R I E P S W A D V K K D L I S Y G G G W K L E G E W K E G E
 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900
 GAAGTCAGGATTGGCACTGGAGCCTGGAAGAAATCCAGAGCGGTCACAAACCTGCTCTTTTCAAAACCAACGCCGGAACATAGGTGCTGTAT
 E V Q V L A L E P G K N P R A V Q T K P G L F K T N A G T I G A V S
 4910 4920 4930 4940 4950 4960 4970 4980 4990 5000
 CTCTGACTTTCTCCTGGAACGTCAAGGATCTCCATATCGACAAAGAAAGGAAAGTTGTGGTCTTTTATGGTAATGGTGTGTGTACAGGAGTGGAGC
 L D F S P G T S G S P I I D K K G K V V G L Y G N G V V T R S G A
 5010 5020 5030 5040 5050 5060 5070 5080 5090 5100
 ATATGTAGTGTATAGCCAGACTGAAGAAAGCATTTGAGACACCCAGAGATCGAGATGACATTTTCGAAAGAGAGACTGACCATCATGGACCTC
 Y V S A I A Q T E K S I E D N P E I E D D I F R K R R L T I M D L

KpnI

NS3

FIGURE 14F

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5110 5120 5130 5140 5150 5160 5170 5180 5190 5200
CACCAGGCGGGAAGACGAGAGTACCTCCGGCCATAGTCAGAGAGCTATAAACGGGTTTGGAGACATTAACTTGGCCCCCAGCTAGAGTTG
H P G A G K T K R Y L P A I V R E A I K R G L R T L I L A P T R V V

5210 5220 5230 5240 5250 5260 5270 5280 5290 5300
TGGCAGCTGAATGGAGGAGCCCTTAGAGACTTCCCAATAAGATACAGACCCCGCCAGCTAGAGCTAGAGACACCGGGGGAGATTGTGGACCTAAT
A A E H E E A L R G L P I R Y Q T P A I R A E H T G R E I V D L H

5310 5320 5330 5340 5350 5360 5370 5380 5390 5400
GTGTCATGCCACATTTACCATGAGGCTGCTATCACCAGTGTAGAGTGCCCAACTACACCTGATTATCATGGACGAGCCCATTTTCACAGACCCAGCAAGT
C H A T F T H R L L S P V R V P N Y N L I I H D E A H F T D P A S

5410 5420 5430 5440 5450 5460 5470 5480 5490 5500
ATAGCAGCTAGAGGATACATCTCAACTCGAGTGGAGATGGGTGAGGAGCTGGGATTTTATGACAGCCACCTCCCCCGGAGACGAGACCCATTTTCCTC
I A A R G Y I S T R V E H G E A A G I F H T A T P P G S R D P F P Q

T

5510 5520 5530 5540 5550 5560 5570 5580 5590 5600
AGAGCAATGCACCAATCATGATGAAGAAAGAGAAATCCCTGAACGCTCGTGGAAATCCGGACATGAATGGTCACGGNTTTAAAGGGAGAGACTGTTTG
S N A P I I D E E R E I P E R S W N S G H E W V T D F K G K T V W

5610 5620 5630 5640 5650 5660 5670 5680 5690 5700
GTTCTCCNAGTATAAAGCAGGAANTGATATAGCAGCTGCTGAGGAAATGGAAGAAAGTGAACAACCTCAGTAGAGACCTTTGATTTCTGAG
F V P S I K A G N D I A A C L R K N G K K V I Q L S R K T F D S E

5710 5720 5730 5740 5750 5760 5770 5780 5790 5800
TATGTCAGACTAGAACCAATGATGGGACTTGGTGTACAACTGACATTTCAAGATGGGTGCCAATTTCAAGCTGAGAGGGTTATAGACCCAGAC
Y V K T R T N D H D F V V T T D I S E H G A N F K A E R V I D P R R

5810 5820 5830 5840 5850 5860 5870 5880 5890 5900
GCTGCATGAAACCACTACTACAGATGTTGAAGAGCGGTGATTTCTGGCAGGACCTATGCCAGTGACCCACTCTAGTCAGACACNAGAGAGGGAG
C H K P V I L T D G E E R V I L A G P H P V T H S S A A Q R R G R

5910 5920 5930 5940 5950 5960 5970 5980 5990 6000
AATAGGAGAAATCCAAATGAGAAATGACCAAGTACATATACATGCGGGAACCTCTCGAATGATGAAGACTGTGCACACTGGAAGAGAACTAAATG
I G R N P K N E N D Q Y I Y H G E P L E N D E D C A H W K E A K H

6010 6020 6030 6040 6050 6060 6070 6080 6090 6100
CTCTAGATAACATCAACCGCCAGAGGAATCATTTCTAGCATGTTCCAAACCAAGAGGTGAAGGTGATGCCATTGATGCCGAATACCGCTTGAGAG
L L D N I N T P E G I I P S M F E P E R E K V D A I D G E Y R L R G

FIGURE 14G

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7010 7020 7030 7040 7050 7060 7070 7080 7090 7100
CCTCAGTGAATGTGTCCTAACAGCTATAGCCCAACCCACAGCTGTTAATGGGTCTCGGGAAGGATGGCCATTGTCAAAAGATGGACATCGGAGTCC
S V N V S L T A I A N Q A T V L H G L G K G W P L S K H D I G V P

7110 7120 7130 7140 7150 7160 7170 7180 7190 7200
CCTTCTCGCCATGGATGCTACTCACAAGTCAACCCCATAACTCTCACAGCAGCTCTTTTCTATTGGTAGCACCATTATGCCATCATAGGGCCAGGACTC
L L A I G C Y S Q V N P I T L T A A L F L L V A H Y A I I G P G L

7210 7220 7230 7240 7250 7260 7270 7280 7290 7300
CAAGCAAAAGCAACCCAGAGCTCAGAAAGAGCGCGGGGCATCTGAAACCCCACTGTGATGGGAATAACAGTGAATGACCTAGATCCCATAC
Q A K A T R E A Q K R A A A G I H K N P T V D G I T V I D L D P I P

7310 7320 7330 7340 7350 7360 7370 7380 7390 7400
CTTATGATCCAAAGTTTGAAGAAGCAGTGGGACAAGTAATGCTCTAGTCTCTCGTGACTCAAGTATGATGATGAGGACTACATGGGCTCTGTGTGA
Y D P K F E K Q L G Q V H L L V L C V T Q V L H M R T T W A L C E

7410 7420 7430 7450 7460 7470 7480 7490 7500
GGCTTTAACCTTAGCTACCGGGCCCTCTCCACATGTGGGAAGGAATCCAGGGAGGTTTGGACACACTACCAATTCGGTGTCAATGGCTAACATTTT
A L T L A T G P I S T L W E G N P G R P W N T T I A V S H A N I F

7510 7520 7530 7540 7550
AGAGGGAGTTACTTGGCCGAGCTGGACTTCTCTTTCTATTATGAGAACACACACACAGAGGGGAACCTGGCAACATAGGAGAGACGCTTGGAG
R G S Y L A G A G L L P S I H K N T T N T R R G T G N I G E T L G E

7610 7620 7630 7640 7650 7660 7670 7680 7690 7700
AGAAATGGAAGCCGATGAACGATGGGAAAAGTGAATCCAGATCTACAGAAAAGTGAATCCAGGAACTGGATAGACCTTAGCAAAAGAGG
K W K S R L N A L G K S E F Q I Y K K S G I Q E V D R T L A K E G

7710 7720 7730 7740 7750 7760 7770 7780 7790 7800
CATTAAAGAGGAGAAAGGACCCATCAGCTGTGTCGGAGGCTCAGCAAACTGAGATGGTTCTGTGAGAGAAACATGGTCACACAGAGGGAAGTA
I K R G E T D H H A V S R G S A K L R W F V E R N M V T P E G K V

7810 7820 7830 7840 7850 7860 7870 7880 7890 7900
GTGGACCTCGTTGTGCAGAGGAGGCTGTCTACTATTTGTGGAGGACTAAAGATGAAGAGAGTCAAGGCTCAACAAAGGAGGACCAGCACG
V D L G C G R G G W S Y Y C G G L K N V R E V K G L T K G G P G H E

7910 7920 7930 7940 7950 7960 7970 7980 7990 8000
AAGAACCCATCCCATGTCAACATATGGTGGTGAATCTAGTGGCTCTTCAAGTGGAGTTGACGTTTCTTCTATCCCGCCCAAGAGTGTGACACATTAT
E P I P H S T Y G W N L V R L Q S G V D V F F I P P E K C D T L L

NS

FIGURE 14I

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10010 10020 10030 10040 10050 10060 10070 10080 10090 10100
CAGTCTGGACAGGGTGGATTCAAGAAACCCATGGATGGAGACAAACCTCCAGTGGAAATCCCATCTACTTGGGAAAGAGNAGA
V W N R V W I Q E N P W H E D K T P V E S W E I P Y L G K R E D

HpaI
10110 10120 10130
CCATGGTGGCTCATTTGATTGGTTAAACAGCAGGGCCACCTGGGCAAGAACATCCAGCAGCAATAATCAAGTTAGATCCCTTATAGGCAATGAA
Q W C G S L I Q L T S R A T W A K N I Q A A I N Q V R S L I G N E

3'-NC
10210 10220 10230 10240 10250 10260 10280 10290 10300
GAATACACAGATTACATGCCCATCCATGAAAGATTTCAGAGAGACAGGAGCAGGAGTTCTGTGTAGAAAGCAAACTAACATGAACAAGGCTA
E Y T D Y H P S M K R F R R E E E A G V L W

10310 10320 10330 10340 10350 10360 10370 10380 10390 10400
GAAGTCAGGTCGGATTACCCCATAGTACGGAAATAACTATGCTACCTGTGAGCCCCGTCCAGGACGTTAAAGAGAGTCAGGCCATCATTAATGCCATAG

10410 10420 10430 10440 10450 10460 10470 10480 10490 10500
CTTGAGTAARCTATGCAGCCTGTAGCTCCACCTGAGAGGGTGTAAATAATCCGGGAGGCCACAAACCATGGAGCTGTACGCATGGCGTAGTGGACTAGC

10510 10520 10530 10540 10550 10560 10570 10580 10590 10600
GTTAGAGAGAGCCCCCTCCCTTACAAATCGCAGCAGCAATGGGGCCCAAGCGGAGATGAGCTGTAGTCTCGCTGGAAGACTAGAGGTTAGAGAGGAC

10610 10620 10630 10640 10650 10660 10670 10680 10690 10700
CCCCCGAACAANAACAGCATATTGACGCTGGGAAGACCAGAGATCCTGCTGCTCCTCAGCATCATTCAGGCGCACAGAACGCCAGAAATGGAAATG

10710 10720
GTGCTGTGATCAACAGGTTCT-3' Terminus of the Genomic mRNA

CTACAGCATGCTAGGTGATTA = Amplimer CD2-10687.Xba
CTAGATAGGTGATTA = Amplimer CD-10687.X2
XbaI

FIGURE 14L

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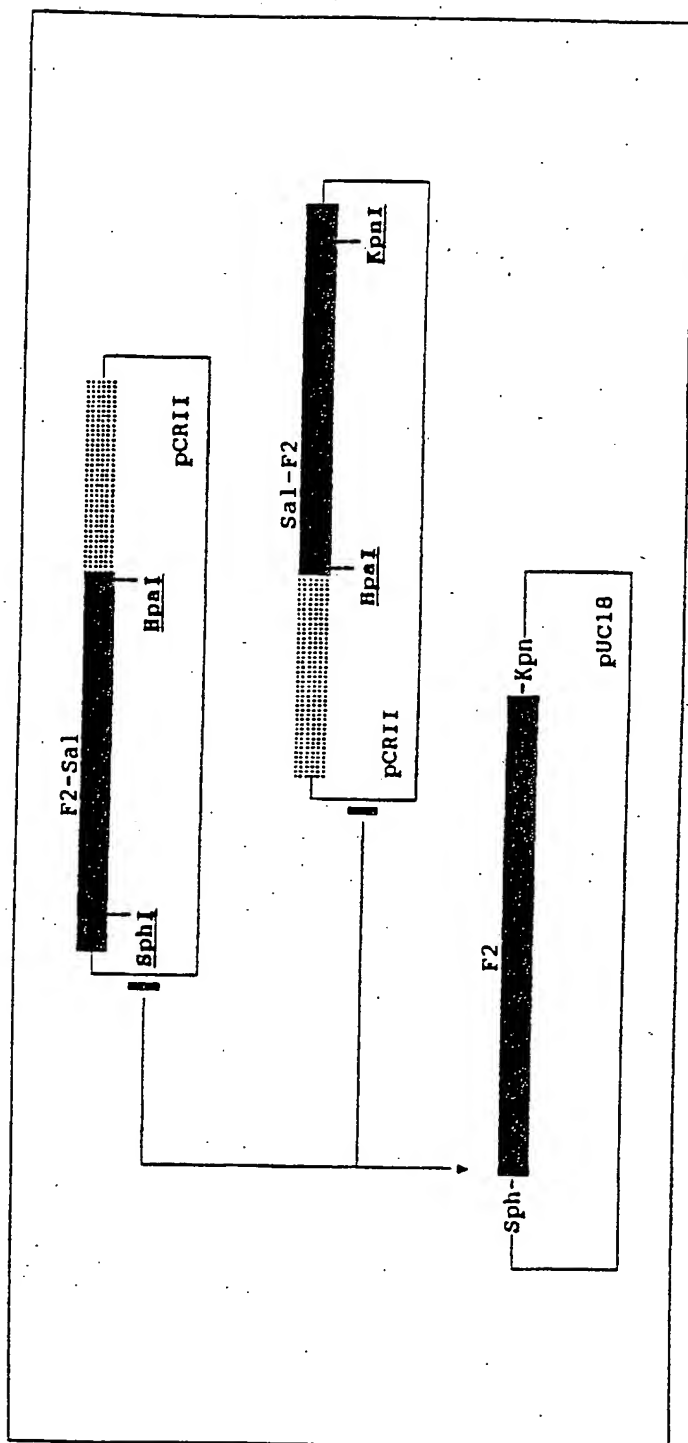


FIGURE 15

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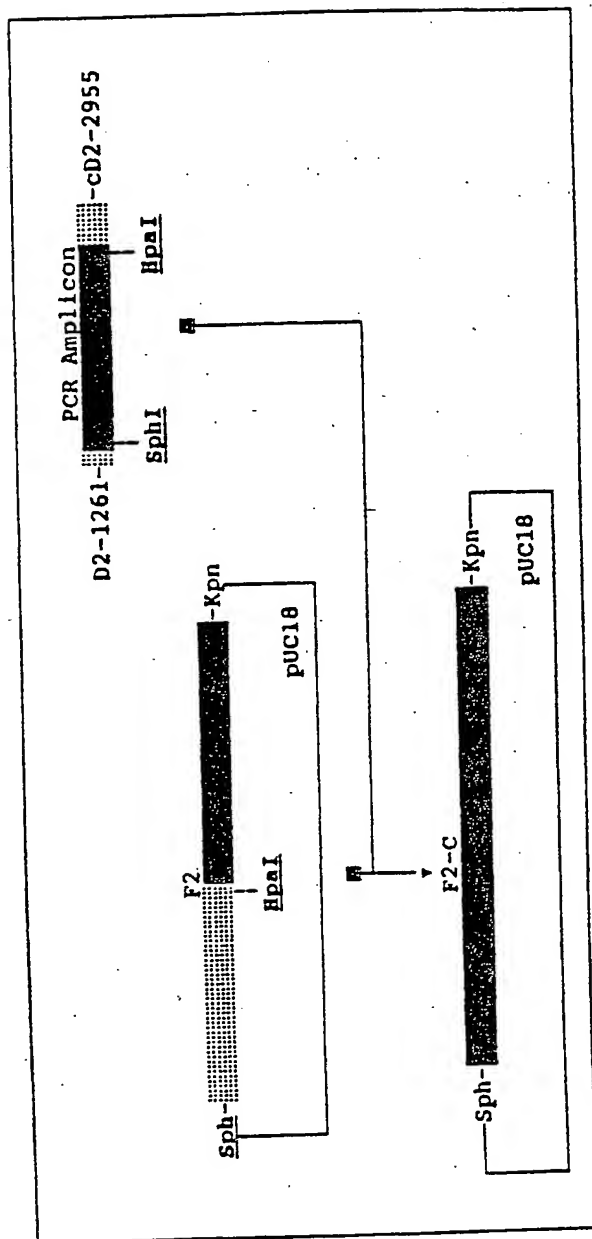


FIGURE 16

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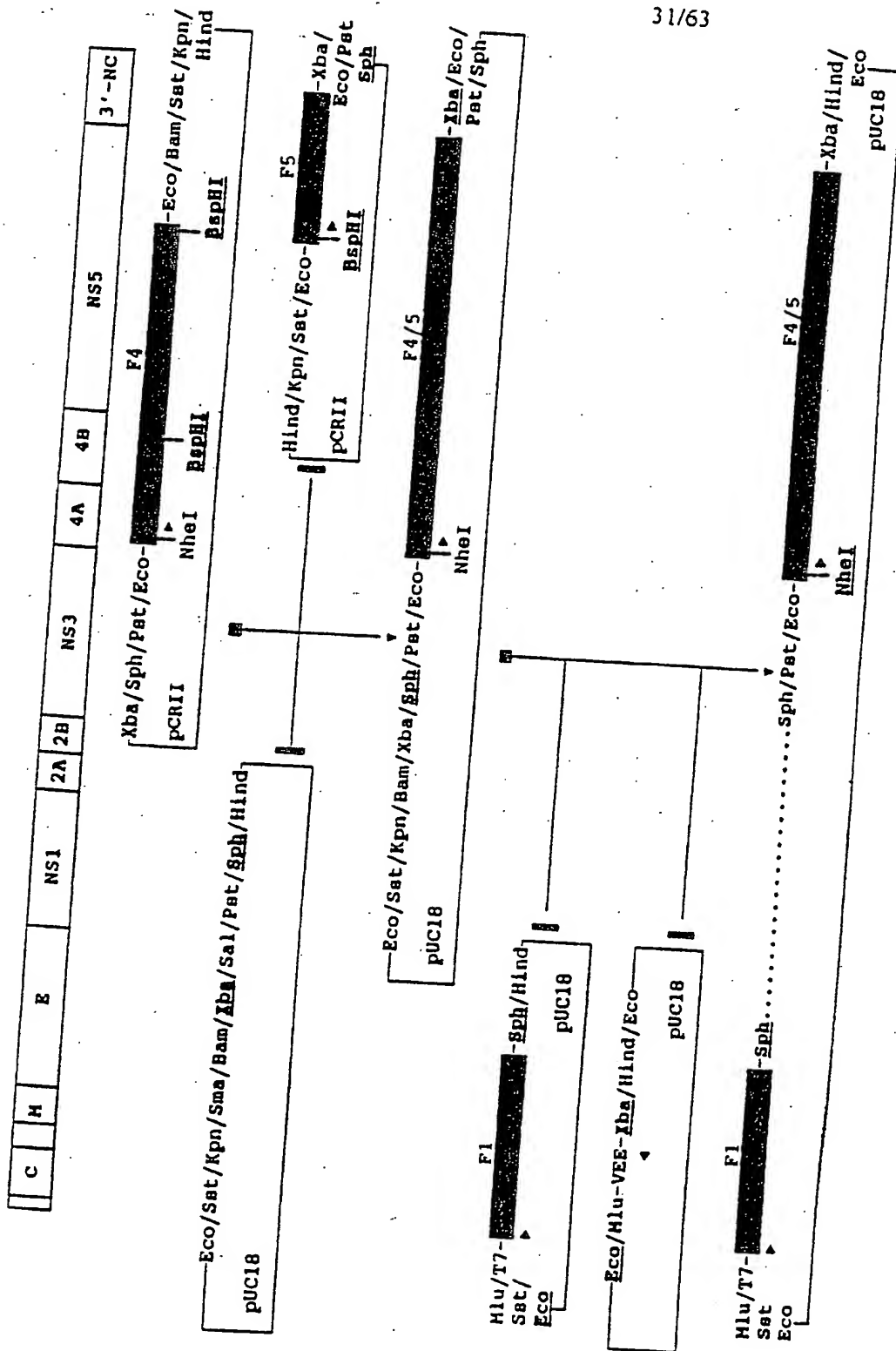


FIGURE 17A

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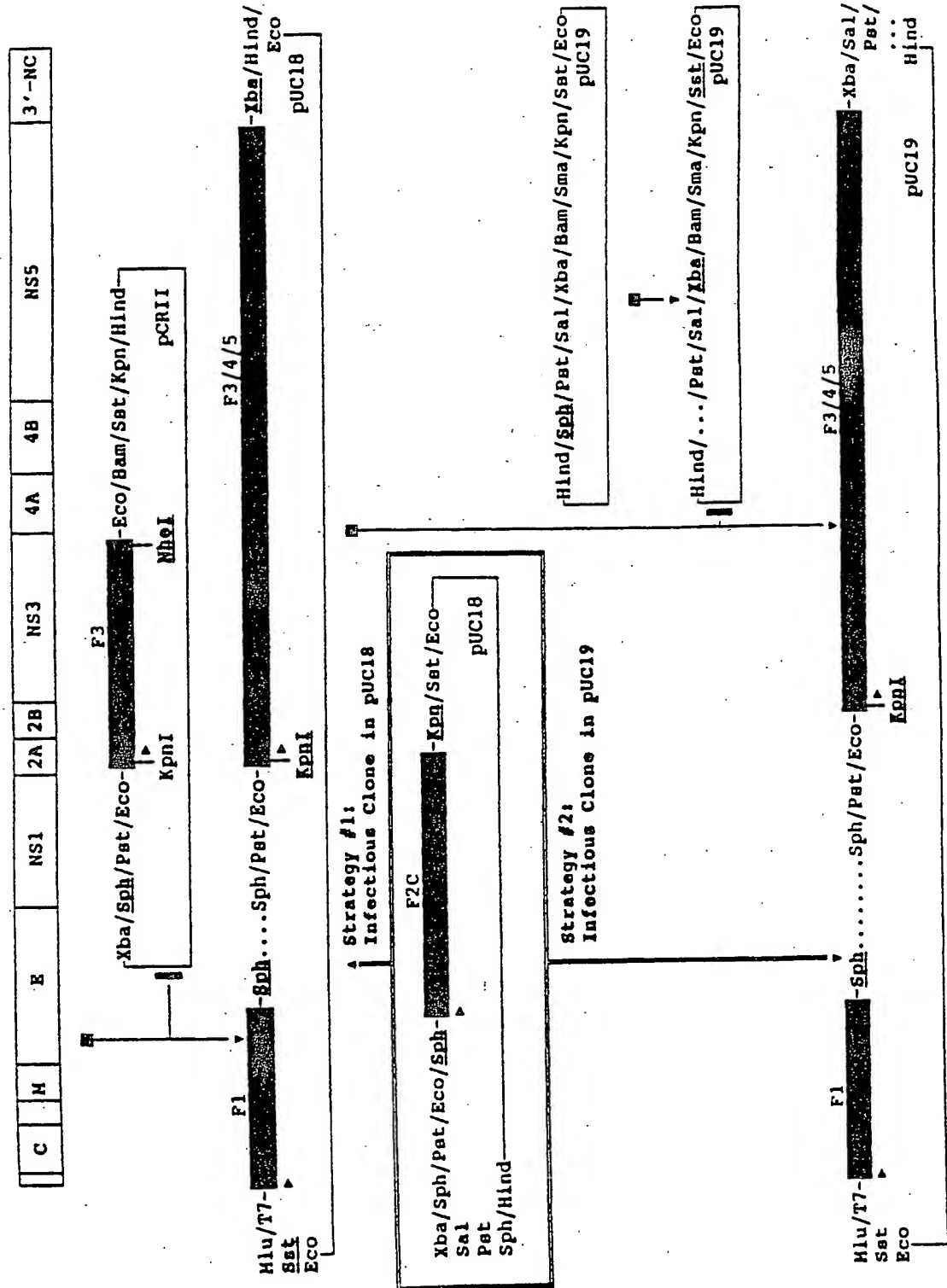


FIGURE 17B

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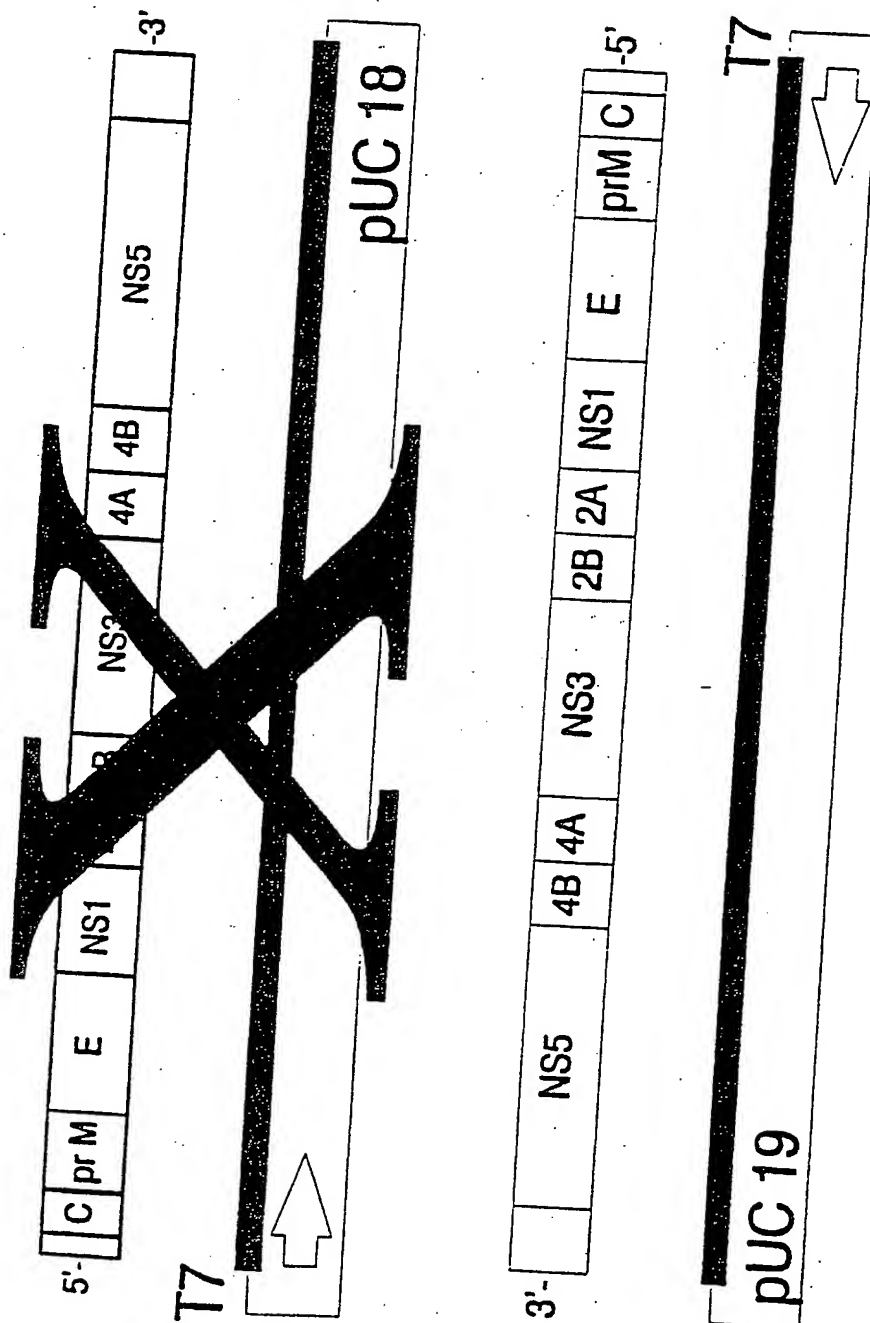


FIGURE 18

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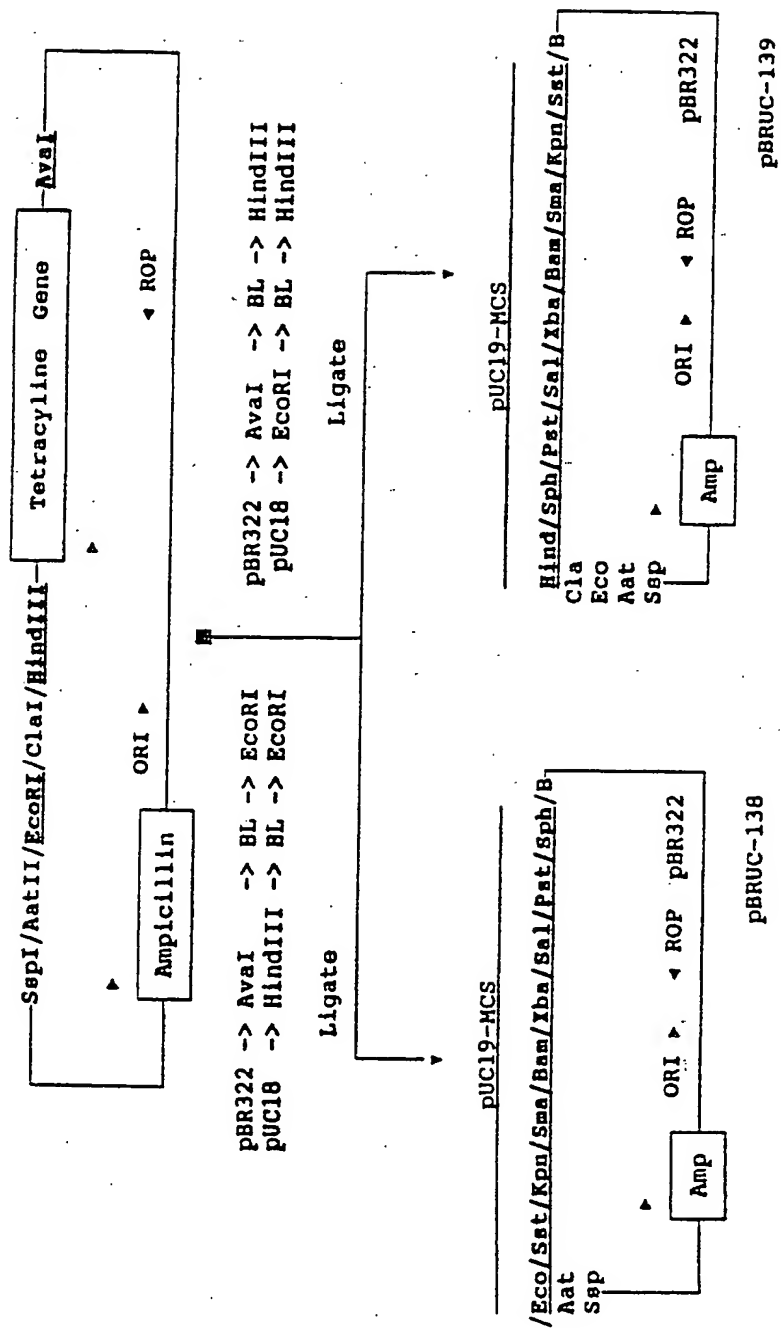


FIGURE 19

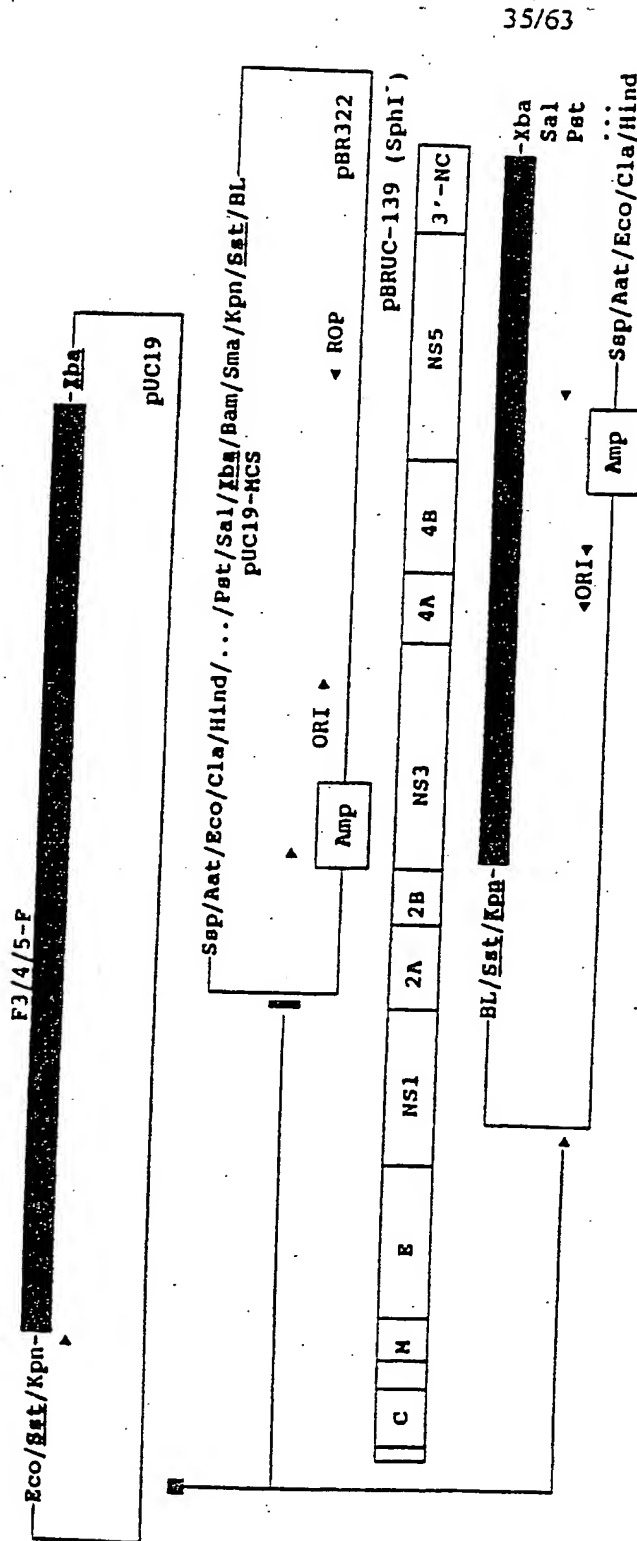


FIGURE 20A

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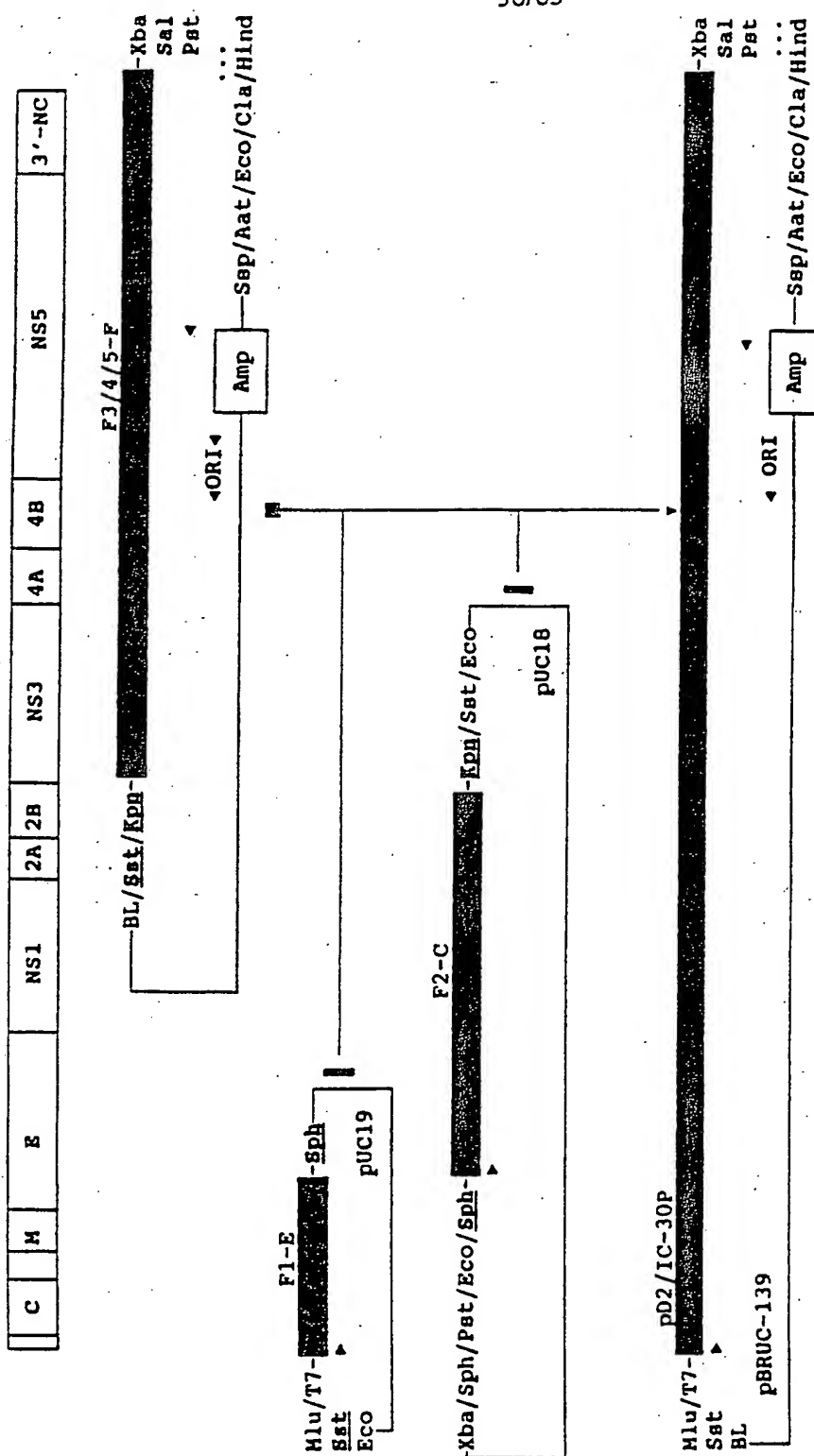


FIGURE 20B

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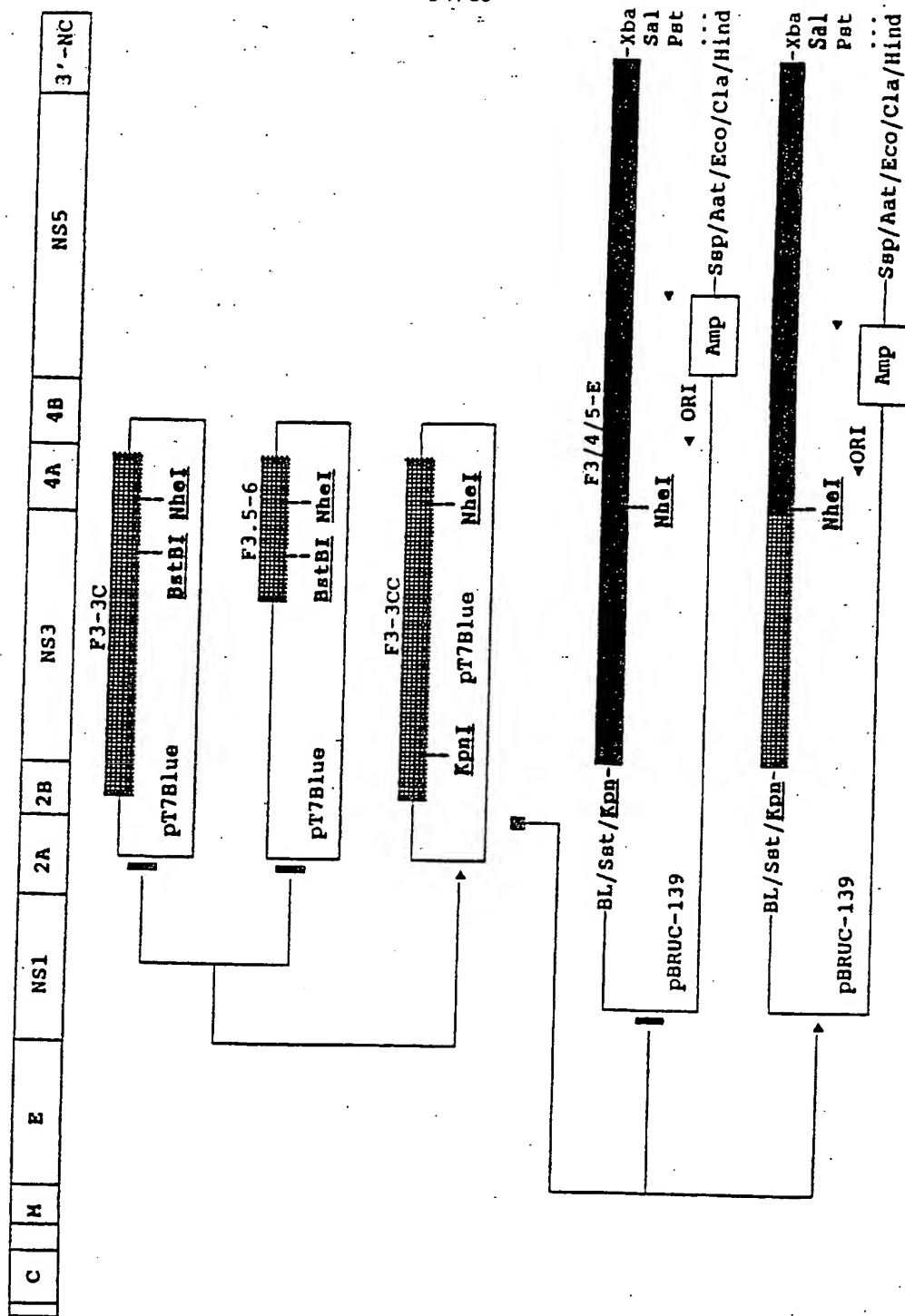


FIGURE 21A

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C	H	E	NS1	2A	2B	NS3	4A	4B	NS5	3'-NC
---	---	---	-----	----	----	-----	----	----	-----	-------

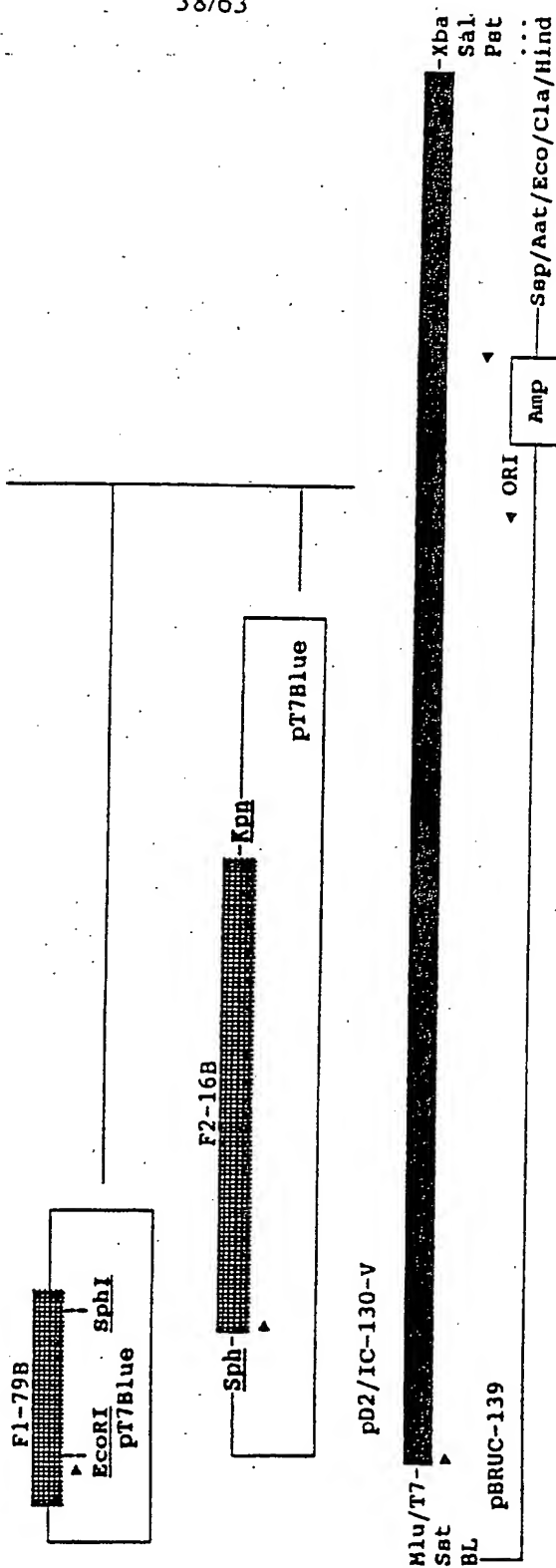


FIGURE 21B

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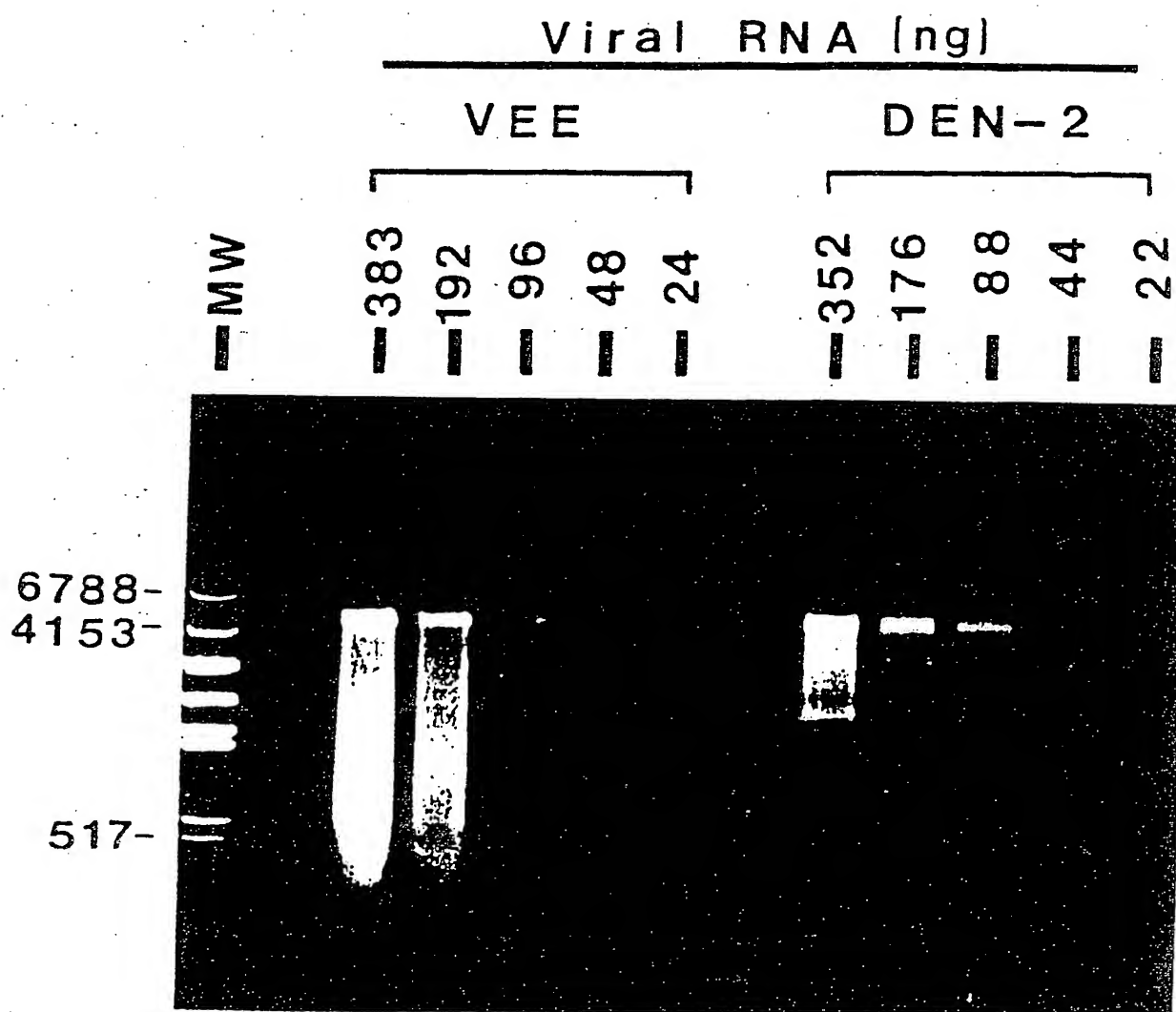


FIGURE 22

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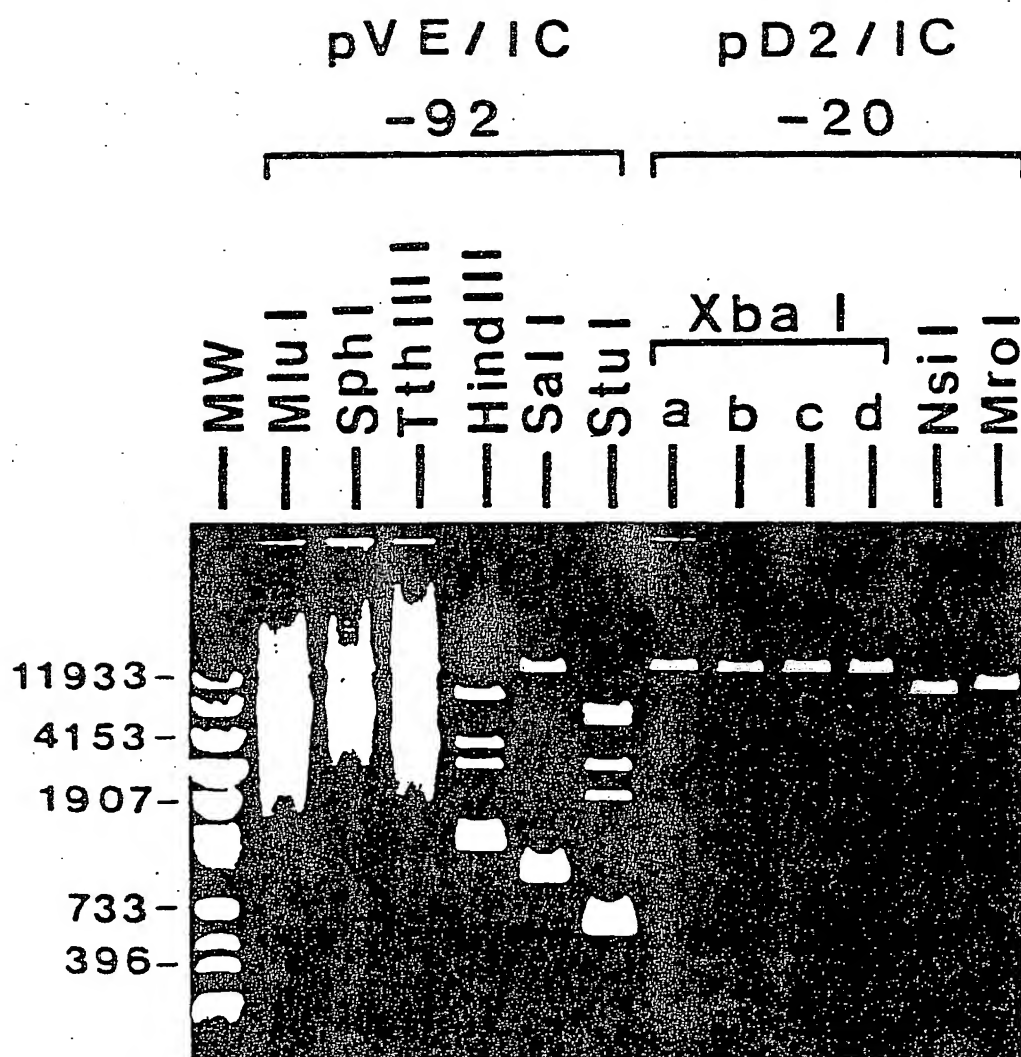


FIGURE 23

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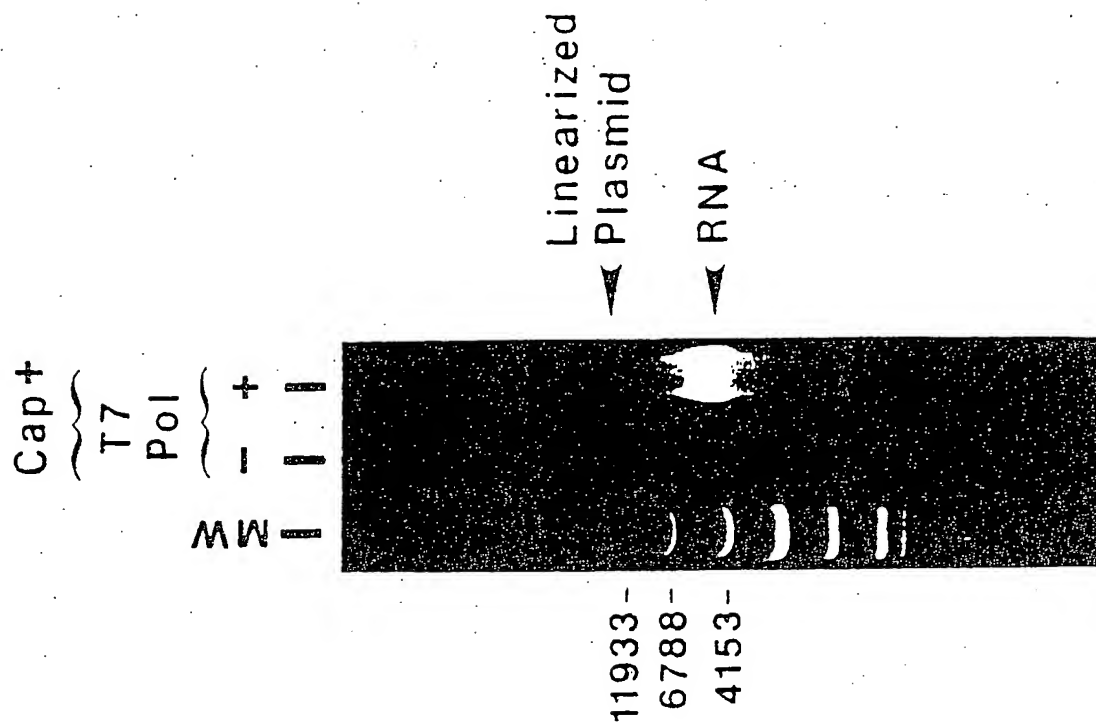


FIGURE 24B

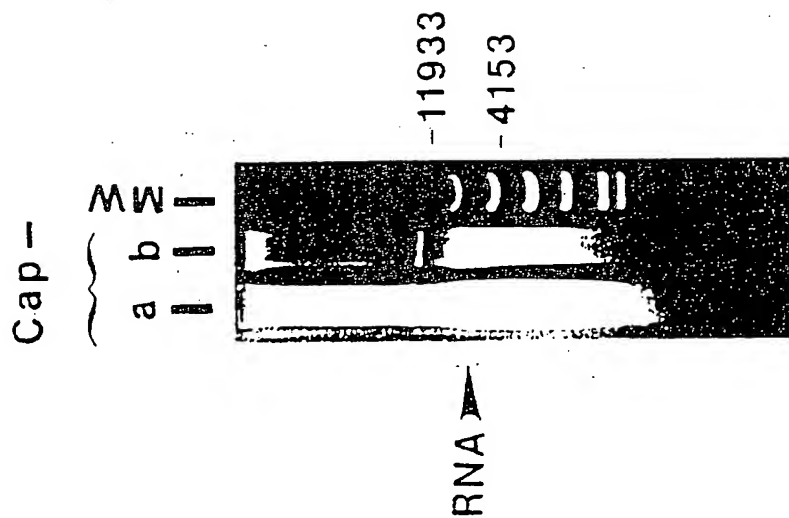


FIGURE 24A

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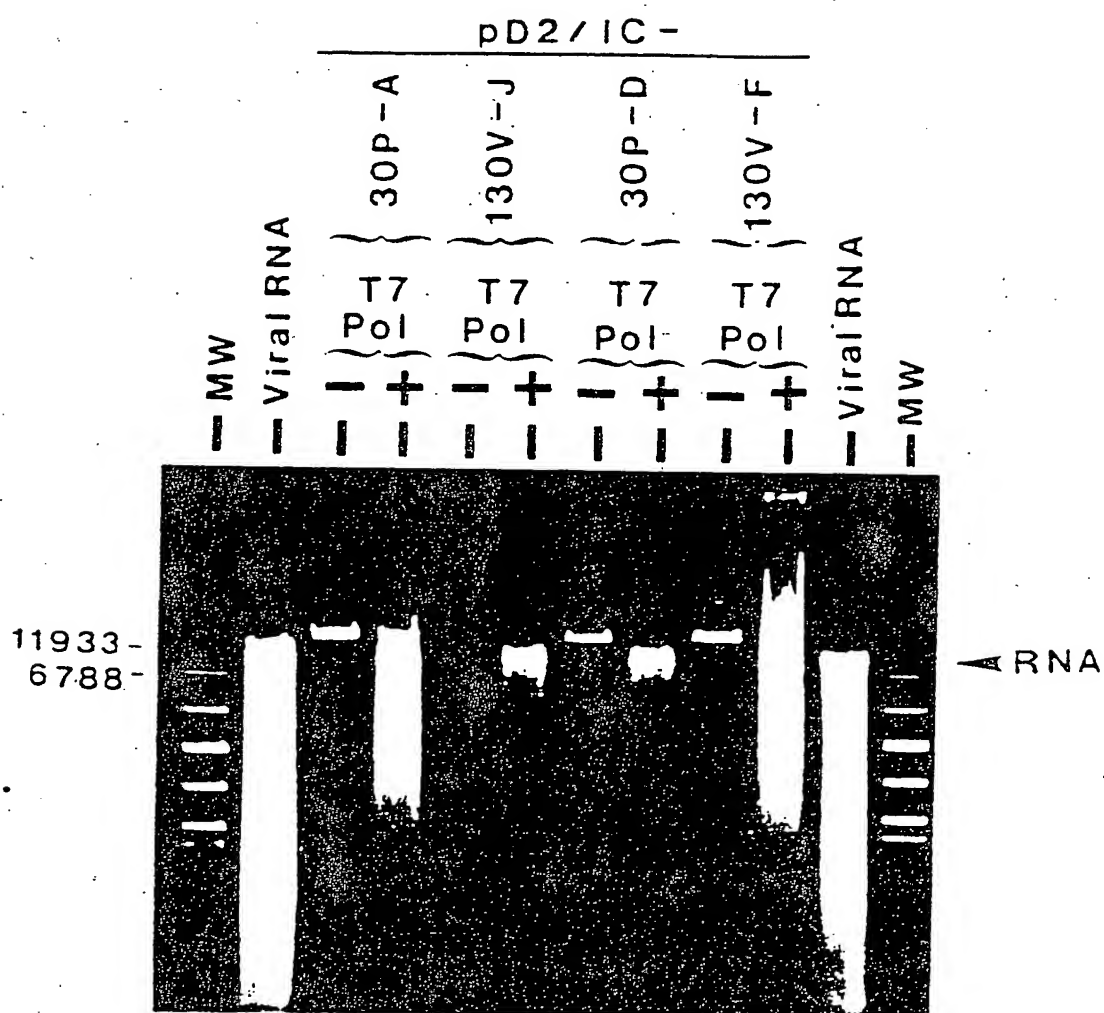


FIGURE 25

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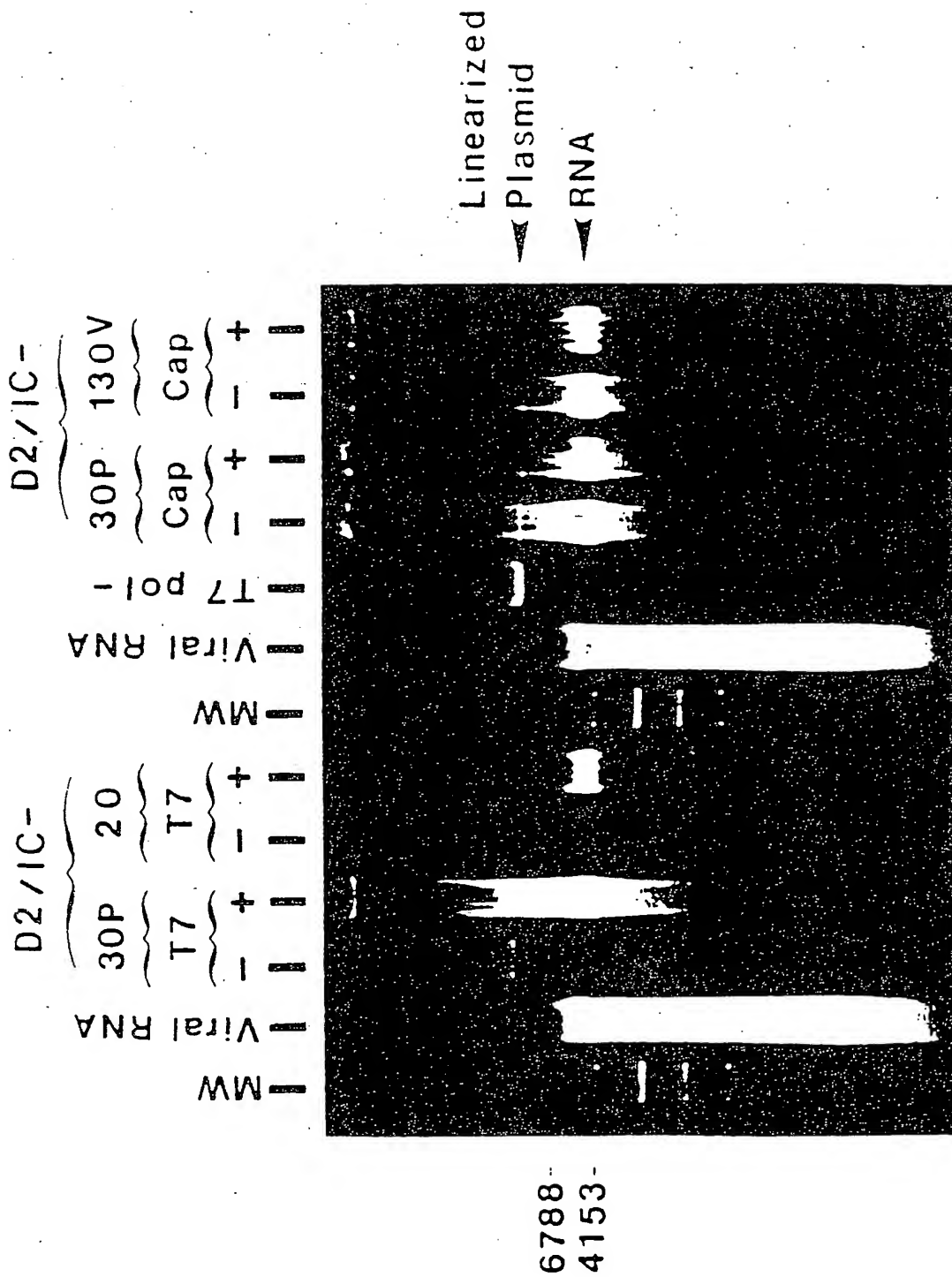


FIGURE 26

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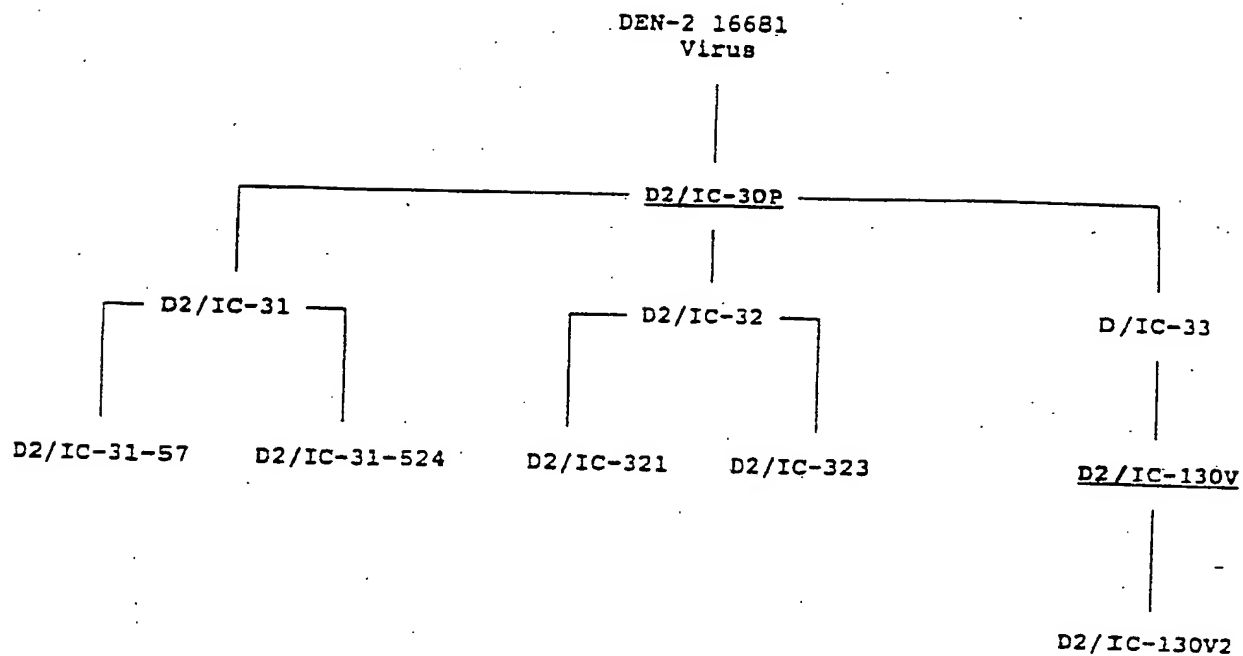
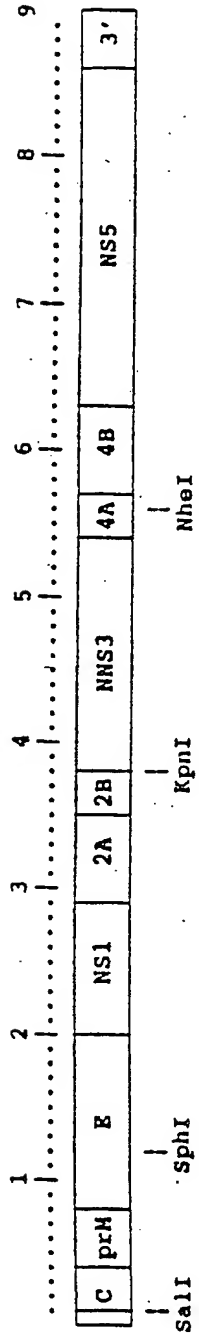


FIGURE 27

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pd2/IC-



FIGURE 28

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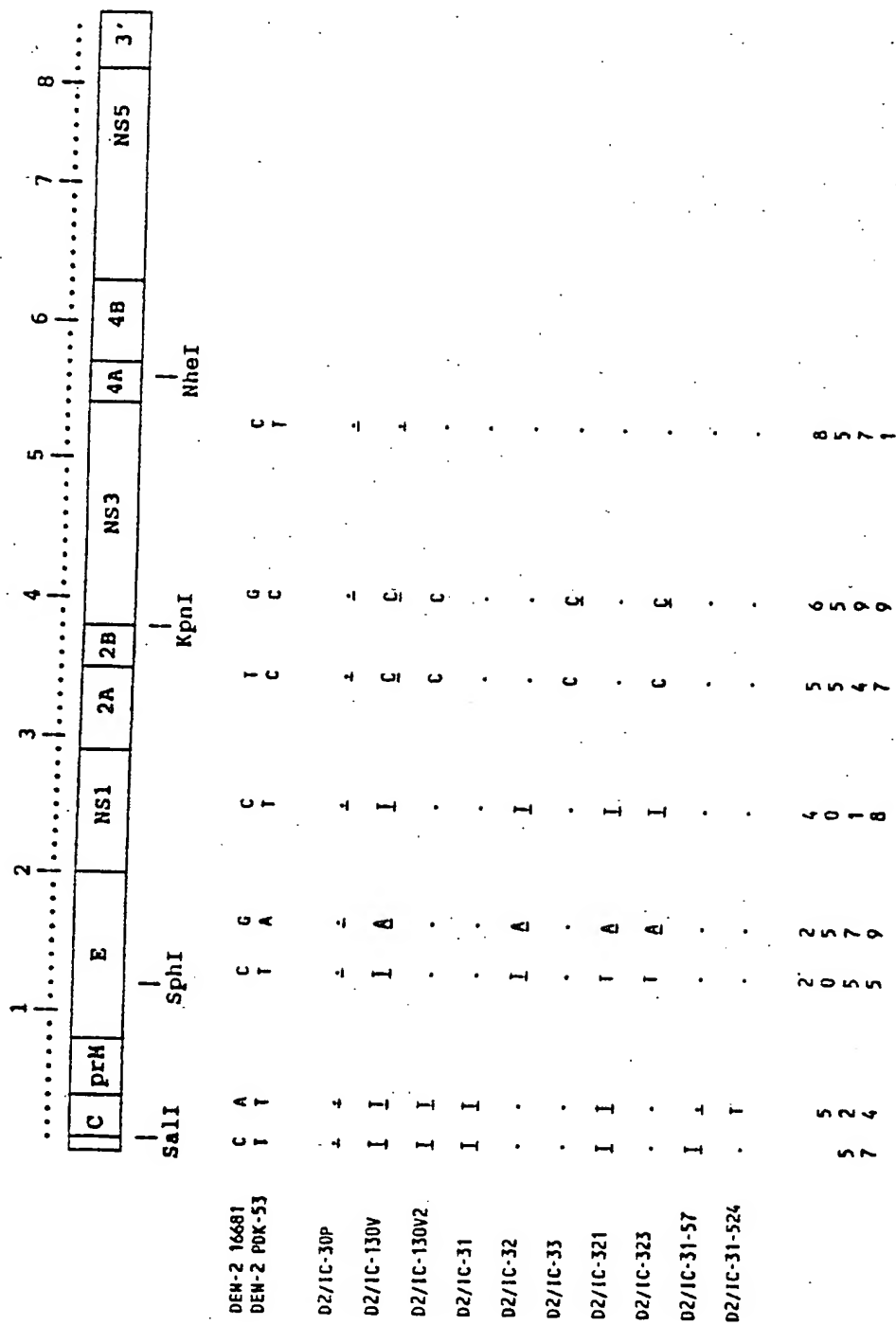


FIGURE 29

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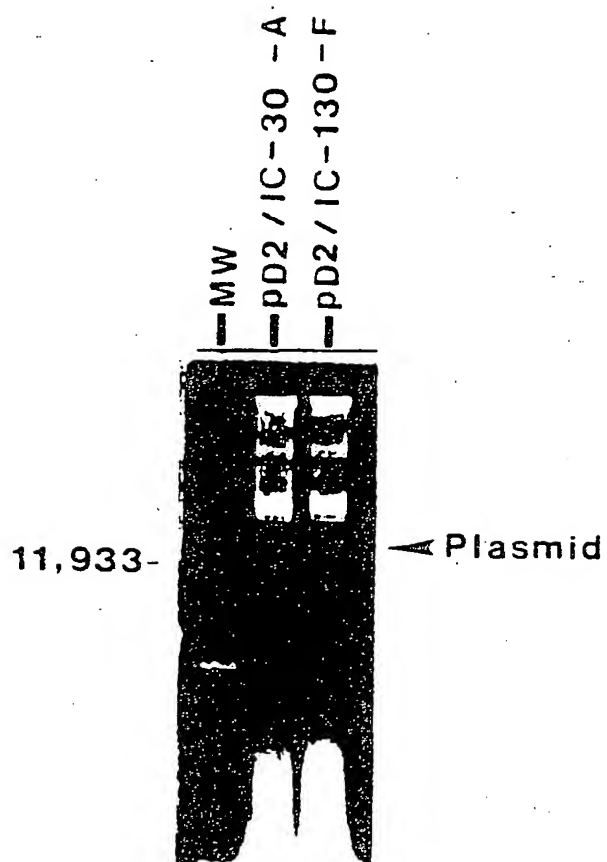


FIGURE 30

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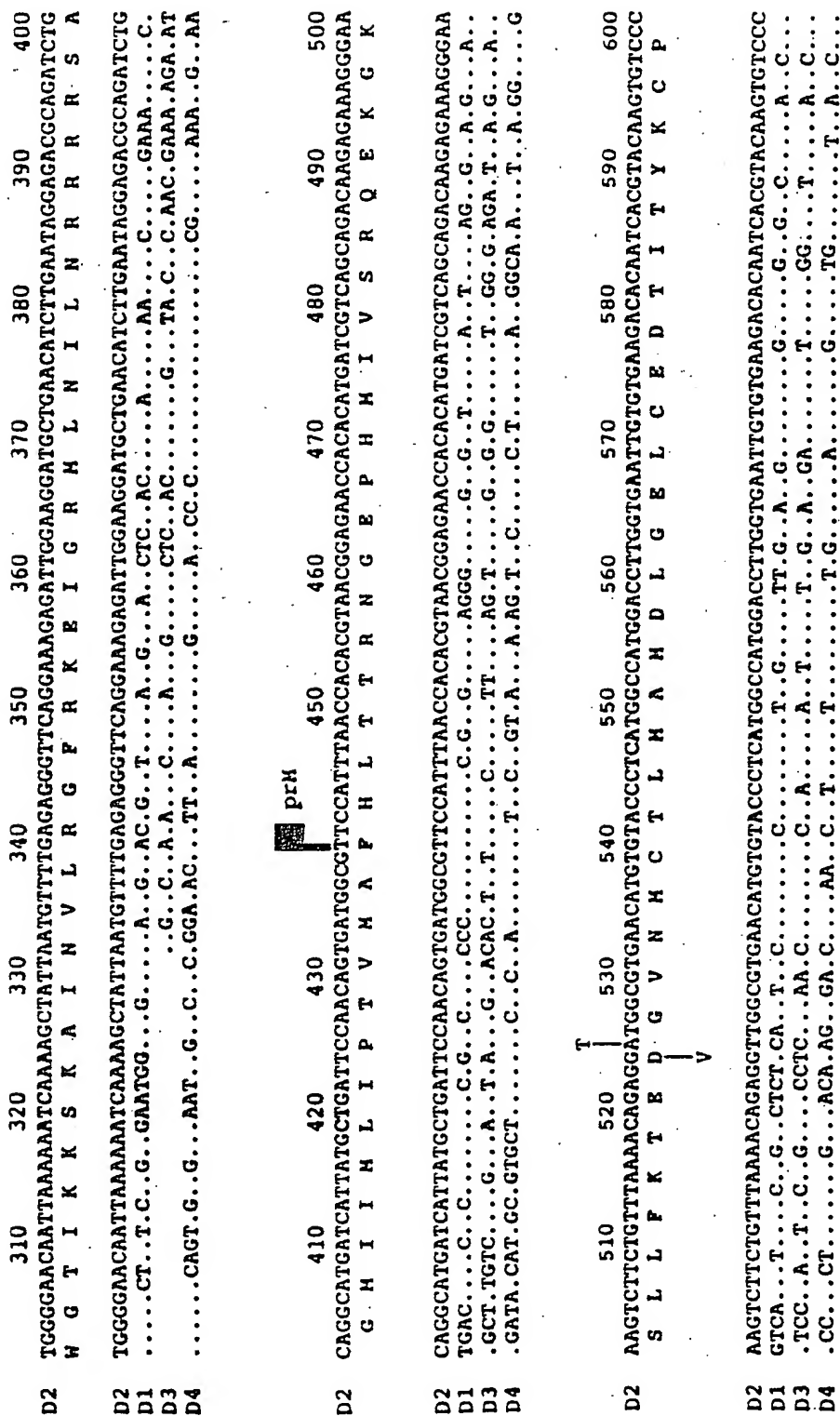


FIGURE 31B

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610 620 630 640 650 660 670 680 690 700
 D2 CTTCTCAGGCAGATGAGCCAGAGACATAGACTGTTGGTGCACCTCTACCTCCACGTGGGTAACTTATGGACGTGTACCAACCATGGGAGAACATAGAA
 L L R Q N E P E D I D C W C N S T S T W V T Y G T C T T H G E H R R

 610 620 630 640 650 660 670 680 690 700
 D2 CTTCTCAGGCAGATGAGCCAGAGACATAGACTGTTGGTGCACCTCTACCTCCACGTGGGTAACTTATGGACGTGTACCAACCATGGGAGAACATAGAA
 D1 .GGA...CTG..GCG..A...T...G.T...TG.C...GA...A...G.C...A...CT.TCA.CT..C...CC..C
 D3 .ACA.T.CCG.AGTG...T...C...CT...A..G..A...G...A..A.C.ATCAAGCT...G...G...C
 D4 T.A..GGTCA.T.CC..A..T...T.T.C...TCTC...T.C...C.A...A.AC...CAG.GC...GG...C

 710 720 730 740 750 760 770 780 790 800
 D2 GAGAAAAGATCAGTGGCAGTGGTCCACATGTTGGGATGGGACTGGAGACAGCAACTGAAACATGGATGTATCATCAGAGGGGCTGGAAACATGTCCN
 E K R S V A L V P H V G M G L E T R T E T W H S S E G A W K H V Q

 710 720 730 740 750 760 770 780 790 800
 D2 GAGAAAAGATCAGTGGCAGTGGTCCACATGTTGGGATGGGACTGGAGACAGCAACTGAAACATGGATGTATCATCAGAGGGGCTGGAAACATGTCCN
 D1 ...C..C.T..C..C...T.G.CC...C...GC.T..C..A..A..A..G.C...G...C..T...T...T...GA.A..
 D3 .C..T..G...GT.A.C...C...T.C...C...C..C...C...GG.T...A..T...G...A...G..
 D4 ...G..GC.C...A..TT.AACA...TCA...T...A..A..G...G...G...T...G...CT..

 810 820 830 840 850 860 870 880 890 900
 D2 GAGAAATGAACTTGGATCTTGAGACATCCAGGCTTACCATGATGGCAGCAANTCCTGGCATACACCATAGAACGACACATTTCCAAAGAGCCCTGATT
 R I E T W I L R H P G F T H M A A I L A Y T I G T T H F Q R A L I

 810 820 830 840 850 860 870 880 890 900
 D2 GAGAAATGAACTTGGATCTTGAGACATCCAGGCTTACCATGATGGCAGCAANTCCTGGCATACACCATAGAACGACACATTTCCAAAGAGCCCTGATT
 D1 A.A.G.A..G...GCTC...A...GG...A..CCTT.T..A...C.TG...AT.CATCAC...G.A..GGA.C..
 D3 ..AGG.A..G..A...GC.C.T..G..C...G.T...AC.A..CCT.T.T..T..CC.TTA...C..TT.CTGAC...G.A..TGG.T..
 D4 ...G.A..G.GC...AC.C...A.C...A..G.GC.CT...G.T.TA...T..T.TG..T..GCA...GC..A.TG.CT.C

 910 920 930 940 950 960 970 980 990 1000
 D2 TTCATCTTACTGACAGCTGTCACTCCTTCAATGACAAATGCGTTGTCATAGGAATGTCAATAGAGACTTGTGGAGGGGTTTCAGGAGGAGCTGGGTTG
 F I L L T A V T P S H T M R C I G H S N R D F V E G V S G S W V D

 910 920 930 940 950 960 970 980 990 1000
 D2 TTCATCTTACTGACAGCTGTCACTCCTTCAATGACAAATGCGTTGTCATAGGAATGTCAATAGAGACTTGTGGAGGGGTTTCAGGAGGAGCTGGGTTG
 D1 ...T..G...TGCTG..A..A..A..T...G.C...A...G.G...AGGC..C...C...AC.G...C...CA...G..
 D3 ..T..AC..T.A.TGCTG..T..C..A..C...A..A..TG...G.AGG...C...T...CC.A..G...CT.CG...C..
 D4 ..TG..C..A...TGCTG...G.C..A..CTACGG...A...G...G.AGG...C...A.C...T...GCA...C..

FIGURE 31C

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```

1410      1420      1430      1440      1450      1460      1470      1490      1500
D2  AGGAAACATGGCAAGGAAATCAAAATACACACAGAGTTCCATCAGAGAGCAGAATTGACAGGTTATGGCACTGTGCACATGAGTCTCTCCACAGA
   G K H G K E I K I T P Q S S I T E A E L T G Y G T V T H E C S P R

1410      1420      1430      1440      1450      1460      1470      1490      1500
D2  AGGAAACATGGCAAGGAAATCAAAATACACACAGAGTTCCATCAGAGAGCAGAATTGACAGGTTATGGCACTGTGCACATGAGTCTCTCCACAGA
   TAC.G.....A.CAACTGCA.CC.....T.AGC.C.T.CGT.G....AT.C.GC....C.AC..C..A..CC.T...T.A..T..T.A..T..G
D3  GCAGGG.GTCACGGCT..G..A-----C..GCA..A.C.G.T....CATT..AC.T.AA.....A..CC..GGGC.A..A.....A...C..G
D4  .TCC..T.....AGTTAC.GC..CG.....T..CAG.TCAC.TCGGGT.....TCA.....C.G.AC.....AGAAC.A...C.C..T..TGAA...C..G

1510      1520      1530      1540      1550      1560      1570      1580      1590      1600
D2  ACGGGCCTCGACTTCAATGAGATGGTGTGCTGCAGATGGAAATAAAGCTTGGCTGGTGCACAGGCAATGGTTCCTAGACCTGCCGTTACCATGTTGC
   T G L D F N E H V L L Q H E N K A W L V H R Q W F L D L P L P W L P

1510      1520      1530      1540      1550      1560      1570      1580      1590      1600
D2  ACGGGCCTCGACTTCAATGAGATGGTGTGCTGCAGATGGAAATAAAGCTTGGCTGGTGCACAGGCAATGGTTCCTAGACCTGCCGTTACCATGTTGC
   ..A..G..A..T..T..C.....ACA...A.....G...T.A.....T..C....AA..G.....T.....T.A..AC.G..T...ACCT
D3  ..A..TT.G..T.....A..A.C.CAT..ACA...A.G..C.....A..A...A..T.A.....T..T...T.A..CC.....ACNT
D4  T.T..AA.T.....T.....A.TC..A..A.A..A...G...A.A...T.....T.A.....TT.G..T..A..TC.....ACAG

1610      1620      1630      1640      1650      1660      1670      1680      1690      1700
D2  CCGGAGCGGACACACAGGGTCARAATTGGATACAGAAAGACACATTTGGTCACTTTCAAAATATCCCATGCCGAGAACACAGGATGTTGTTTACGATC
   G A D T Q G S N W I Q K E T L V T F K N P H A K K Q D V V L G S

1610      1620      1630      1640      1650      1660      1670      1680      1690      1700
D2  CCGGAGCGGACACACAGGGTCARAATTGGATACAGAAAGACACATTTGGTCACTTTCAAAATATCCCATGCCGAGAACACAGGATGTTGTTTACGATC
   T..G..TTTA...TCCAGAG.C.....ACAGAC....TTT.C.....A..T..G.CAG.T.....A.....G.....A..A..C..AC.....
D3  A.....TACAG..G..ACAC...C.....ACAG.....CTTC.T.G..A..T.....G.A.....A..A..G..A..A..A.....C.T.....
D4  A.....A.....TC..A..GTTC.C.....ATT.C.....G.A.....G..A..T..GGT...T.....C....G.....GACA..GC.G.....

1710      1720      1730      1740      1750      1760      1770      1780      1790      1800
D2  CCAAGAGGGGCCATGCACACAGCAGCTTACAGGGGCCACAGAAATCCAAATGTATCAGGAAACTTACTCTTCACAGGACATCTCAAGTGCAGGCTGAGA
   Q E G A H H T A L T G A T E I Q N S S G N L L F T G H L K C R L R

1710      1720      1730      1740      1750      1760      1770      1780      1790      1800
D2  CCAAGAGGGGCCATGCACACAGCAGCTTACAGGGGCCACAGAAATCCAAATGTATCAGGAAACTTACTCTTCACAGGACATCTCAAGTGCAGGCTGAGA
   D1  A.....A..A.....T..G..G..T..A..G.....C.....GG.ACG.CAAC.A..T...G.....C..A..A.....A..A..A..A..A..A..
D3  A.....G..A..A.....T.....G.....A..T.....G.....CC...GG...C.CAAGTA...TG.G..G..CT.A..A..T..A..C..AG
D4  T..G.....A.....TT.T..C..CG.T..A.....G.CG.CTCGGGTGAT.....TCACA.G..TG.....AAG.CC.T

```

FIGURE 31E

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	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900
D2	ATGGACAGCTACAGCTCAAGGATGTCTATCTGTGACACAGGAAGTTTAAAGTTGTGAAGGAATAGCAGAAACACAAACATGGAACATAGTTA									
	H D K L Q L K G H S Y S M C T G K F K V V K E I A E T Q H G T I V I									
D2	ATGGACAAGCTACAGCTCAAGGATGTCTATCTGTGACACAGGAAGTTTAAAGTTGTGAAGGAATAGCAGAAACACAAACATGGAACATAGTTA									
D1A...ACTT.A.....G.....TGTC.....CTCA..C..GT.A.A...A...G.G..T..G..C..G.....TG.TC.GG									
D3AT.GG.A.....G...AGC..TG.A.....TTG..T.GC...GTGT.GAA...A...G.CT.C...G.G...G.....C.C..									
D4G..AT.GAGNA.....G.....A.G.....TT.....CTC.A...AC..A..G..G.....G.....G.....C.....C.....GG									
	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000
D2	TCAGAGTGCATATGCAAGGGGACGGCTCTCCATGCAAGATCCCTTTGAGATATGGATTGGAAAAAAGACATGTCTTAGGTGCGCTGATTACAGTCRA									
	R V Q Y E G D G S P C K I P F E I M D L E K R H V L G R L I T V N									
D2	TCAGAGTGCATATGCAAGGGGACGGCTCTCCATGCAAGATCCCTTTGAGATATGGATTGGAAAAAAGACATGTCTTAGGTGCGCTGATTACAGTCRA									
D1	..GCAG..TA.....AACA.A.G.A.....T..C...TC..CCCA..GA.A..GG.GC.ACCCAAGAT..GA.AT.A.A...C...									
D3	..T.AG..TG.G..CA.....A.A.ATG.A..C.....T.....CTCC.CGGA.....GGAC..GG..A.GC.CA.AAT..CA.A.....C.....C...									
D4	..G.A...CA.G.....T.CT..AG...G...T..AG...CA.A.....GA...G..A.C..G.A.A..GG.T..G..TA.C..CT..TC..C									
	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100
D2	CCCAATGTGACAGAAAAGATAGCCCGAGTCAACATAGNAGCAGAACCTCCATTCCGGAGACAGCTACATCATCATAGGAGTAGAGCCGGACAACTGAAG									
	P I V T E K D S P V N I E A E P P F G D S Y I I I G V E P G Q L K									
D2	CCCAATGTGACAGAAAAGATAGCCCGAGTCAACATAGNAGCAGAACCTCCATTCCGGAGACAGCTACATCATCATAGGAGTAGAGCCGGACAACTGAAG									
D1	..C.A..C..T..C...A.AA.....T..T..G.....A.C.....T..G.....G.GG.....C..GTGAAA..GCTT....A									
D3	..T..G.G.....CA.G..G..GGAG..T.....T..G..T.....T.....A..TA...AG.A..T...A.T.GAGACAA.GCC.....A									
D4	...TT.G.CTGAG.T.CCA.C..TG..AC.....GTT.....C.C.....G.....AG.G.....T..T.GAAACA.TGC.T.A.CA									
	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200
D2	CTCAACTGGTTTAAAGAAAGGAGTTCTATCGGCCCAATGTTTGAACACAACTAGGGGGGGGGGAGAGAGATGGCCATTTTAGGTGACACAGCCTGGGATT									
	L N W F K K G S S I G Q H F E T T M R G A K R H A I L G D T A H D F									
D2	CTCAACTGGTTTAAAGAAAGGAGTTCTATCGGCCCAATGTTTGAACACAACTAGGGGGGGGGGAGAGAGATGGCCATTTTAGGTGACACAGCCTGGGATT									
D1	..A.G.....C.....CAGC..A..GA.....AG...TGCC.A..A..ACGA..G.....C.G..A.....C.A.....C.									
D3	A.....AC.....G.....C..G..T..GA.G.....C..G..T..TCC..A..T..A.G.C.C.....C.G..A.....C.....C.									
D4	...C.T.....C.G.....G.....C..T..A.G.....T.C...TAC..A..T..A.AC.....C.....A.....T.....									

FIGURE 31F

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2210 2220 2230 2240 2250 2260 2270 2280 2290 2300
 D2 TTGGATCCTTGGGAGGAGTGTTTACATCTATAGGARAGGCTCTCCACCAAGTCTTTGGAGCAATCTATGGAGCTGCCCTTCAGTGGGGTTTCATGGACTAT
 G S L G G V F T S I G K A L H Q V F G A I Y G A A F S G V S W T H
 D2 TTGGATCCTTGGGAGGAGTGTTTACATCTATAGGARAGGCTCTCCACCAAGTCTTTGGAGCAATCTATGGAGCTGCCCTTCAGTGGGGTTTCATGGACTAT
 D1 .C..T..TA.A.....C..G.....G.....ACTGG.A.....G..T.....A.TGCA.....T.TG..T..C..A.....T.....C..
 D3AG.....T..T..G.AT..AT..G..AATGG.....A.A.....GAGTGCT..CAC...CCTA..TG....A..C..C.....TG..
 D4T..G.T..T..C.....C.....AT.G.....G.G.....G.T.....AGTG.G...AC.A.CATG..TG.A..A..C.....TG..
 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400
 D2 GAAATCCTCATAGGAGTCATTATCACAATGGATAGGATGAATTCACGCAGCACCTCAGTCTCTGTGACACTAGTATTGGTGGGAATTGTGACACTGTAT
 K I L I G V I I T W I G H N S R S T S L S V T L V L V G I V T L Y
 D2 GAAATCCTCATAGGAGTCATTATCACAATGGATAGGATGAATTCACGCAGCACCTCAGTCTCTGTGACACTAGTATTGGTGGGAATTGTGACACTGTAT
 D1AGGA.....GA.TC.GC.G.....C.....T.A.....A.G.A..G..C..T..G....TGTC.A.CGCA..T..C..G..C.....C
 D3TGA.....T..C..CT.A..C.....GT.....C...AAA..AT..T..TA....AT..TT..TGCA.CGC.A.A.....CA.T.....C..
 D4 T.G.....A..T..GT..C..AG.GTTG.....T..C.C..C...A.G.A..T...A..G..A....GTGCA..GCT..T...GGAA.C..T.....T..
 2410 2420 2430 2440 2450 2460 2470 2480 2490 2500
 D2 TTGGGAGTCATGGTGCAGGCGCATAGTGGTTCGGTTGTGAGCTGGAAACAAAGAACTGAATGTGGCAGTGGGATTTTCATCAGACACACGTCACACA
 L G V H V Q A D S G C V V S W K N K E L K C G S G I F I T D N V H T
 D2 TTGGGAGTCATGGTGCAGGCGCATAGTGGTTCGGTTGTGAGCTGGAAACAAAGAACTGAATGTGGCAGTGGGATTTTCATCAGACACACGTCACACA
 D1 C.A.....T.....A...TCG..A..T..AA.C.A.....GG..G.....T.....A..C..C.....TG.....TA.TG.A..T....
 D3 C.....C.G.....A..T..C.TG..G..T..CA.A.A.....GG.....C.....A.....A.....
 D4 C....CT....CA..T..A..A..G.TG.....T..G...TCA....GTGGG.....T...GG

FIGURE 31G

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2510 2520 2530 2540 2550 2560 2570 2590 2600
 CATGGACAGAACATACAGTTCCCAACCCAGATCCCTTCCTCAAACTAGCTTCAGCTATCCAGAAAGCCCATGAGAGGGCATTTCGTGGAATCCGCTCAGT
 W T E Q Y K F Q P E S P S K L A S A I Q K A H E E G I C G I R S V
 A
 D

D2 CATGGACAGAACATACAGTTCCCAACCCAGATCCCTTCCTCAAACTAGCTTCAGCTATCCAGAAAGCCCATGAGAGGGCATTTCGTGGAATCCGCTCAGT
 D1 .T.....G.....A.....GG.T..C.....CAAG.G....T.AG.....C..TGG...G..ATGG...G....GTG.G
 D3
 D4

HpaI
 2610 2620 2630 2640 2650 2660 2670 2680 2690 2700
 AACAGACTGGAGAACTGATGTGGAAACAAATAACACCCAGAAATTGAATCACAATTCATCAGAAATGAGGTGAAGTTAACTATTATGACAGGGACATC
 T R L E N L H W K Q I T P E L N H I L S E N E V K L T I H T G D I

FIGURE 31H

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FIGURE 32A

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D2	510	520	530	540	550	560	570	580	590	600
D1	LP	GN	AD	TO	GS	NH	IQ	KE	TL	VT
D3	TS	..	L	SQ	ET	NR	QDL	..	TA	..
D4	TA	..	SE	VH	NY	..	RM	..	V	..
D2	610	620	630	640	650	660	670	680	690	700
D1	VIR	QY	EG	DS	PC	KIP	FE	IH	DL	EH
D3	L	K	E	K	..	KDA	..	STE	..	QK
D4	VK	K	..	A	..	A	..	V	..	I
D2	710	720	730	740	750	760	770	780	790	800
D1	DF	GS	LG	GV	FT	SI	GN	AL	HQ	VE
D3	..	I	..	H	..	LV	..	TA	..	VL
D4	V	..	LN	L
D2	810	820	830	840	850	860	870	880	890	900
D1	HT	WE	QY	KF	QPE	SP	SK	LA	SA	IQ
D3
D4

FIGURE 32B

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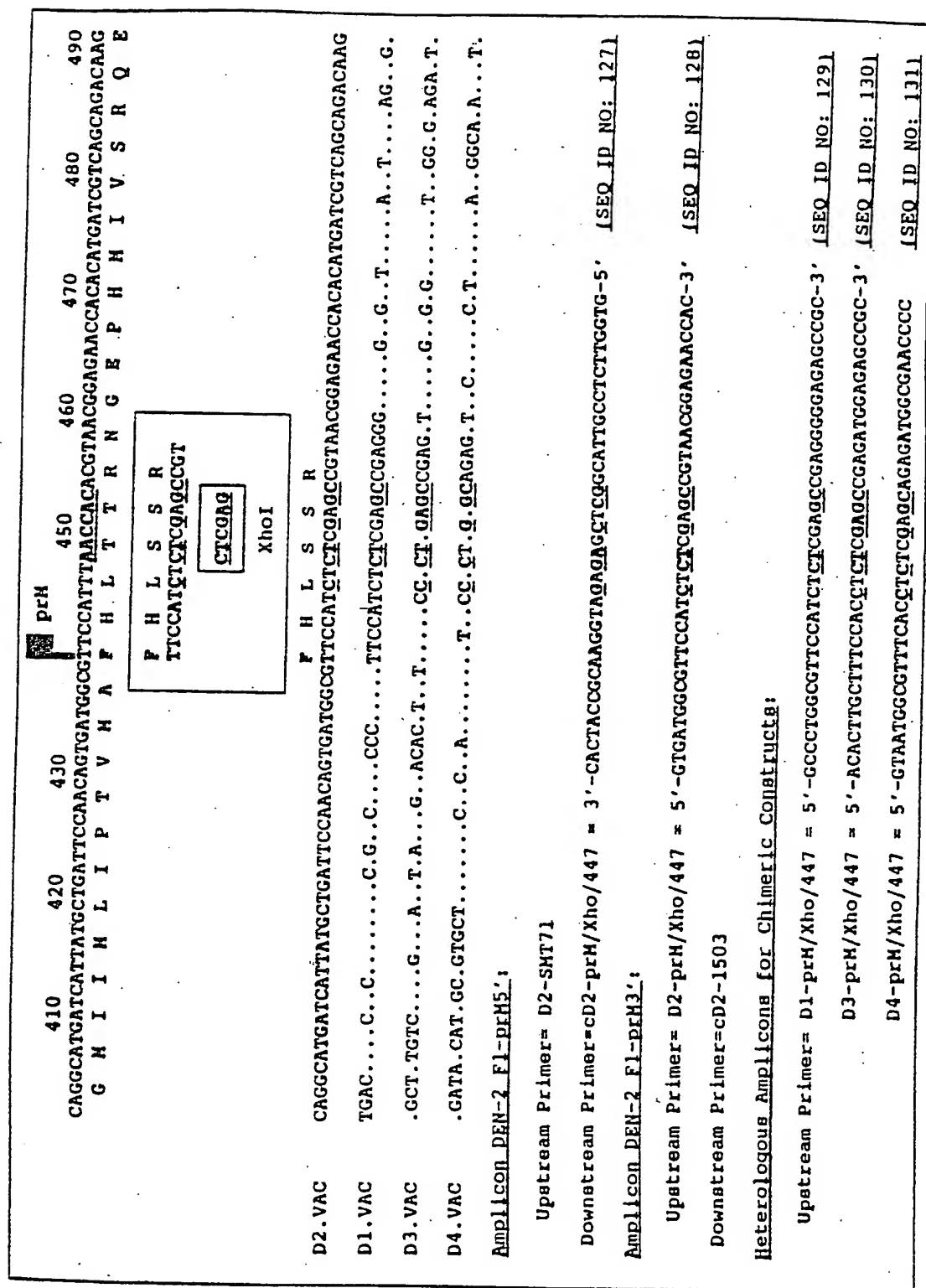


FIGURE 33

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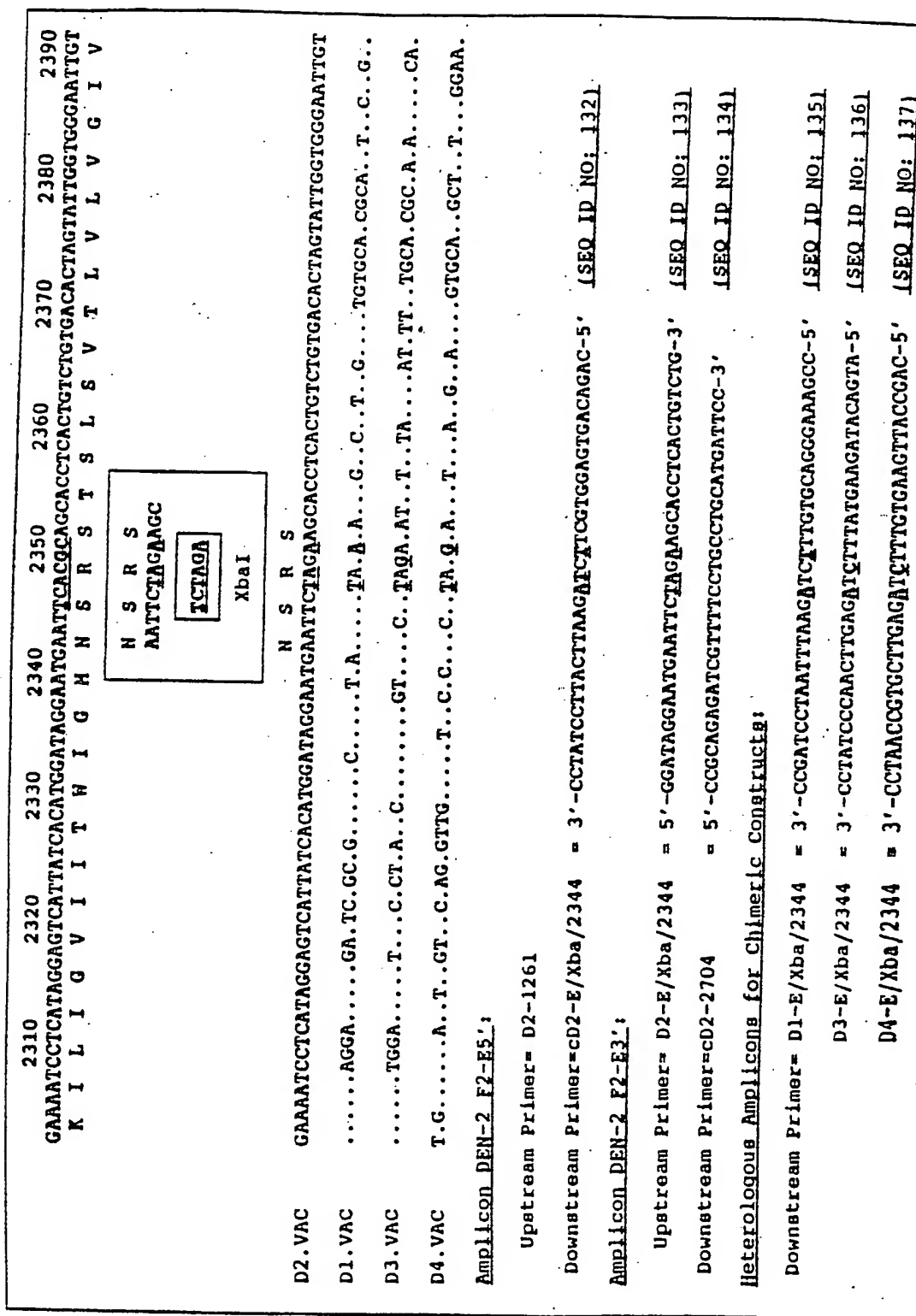


FIGURE 34A

	2410	2420	NS1	2430	2440	2450	2460	2470	2480
D2. VAC	TTGGGAGTCATGGTGCAGGCCGATAGTGGTTGCGTTGTGAGCTGGAGAAACAAAGAACTGAATGTGGCAGTGGGATTTTCATGCACA								
D1. VAC	C.A.....T.....A...TCG.A..T.AA.C.A.....GG.G.....T.....A.C.C.....TG.T....								
D3. VAC	C.....C.G.....A..T..CTG..G..T..CA.A.A.....GG.....C.....A.....A.....								
D4. VAC	C....CT...CA..T.A.A.A..G.TG.....T.G...TCA....GTGGG.....T...GG								
	L G V H V Q A D S G C V V S W K N K E L K C G S G I F I H T								

FIGURE 34B

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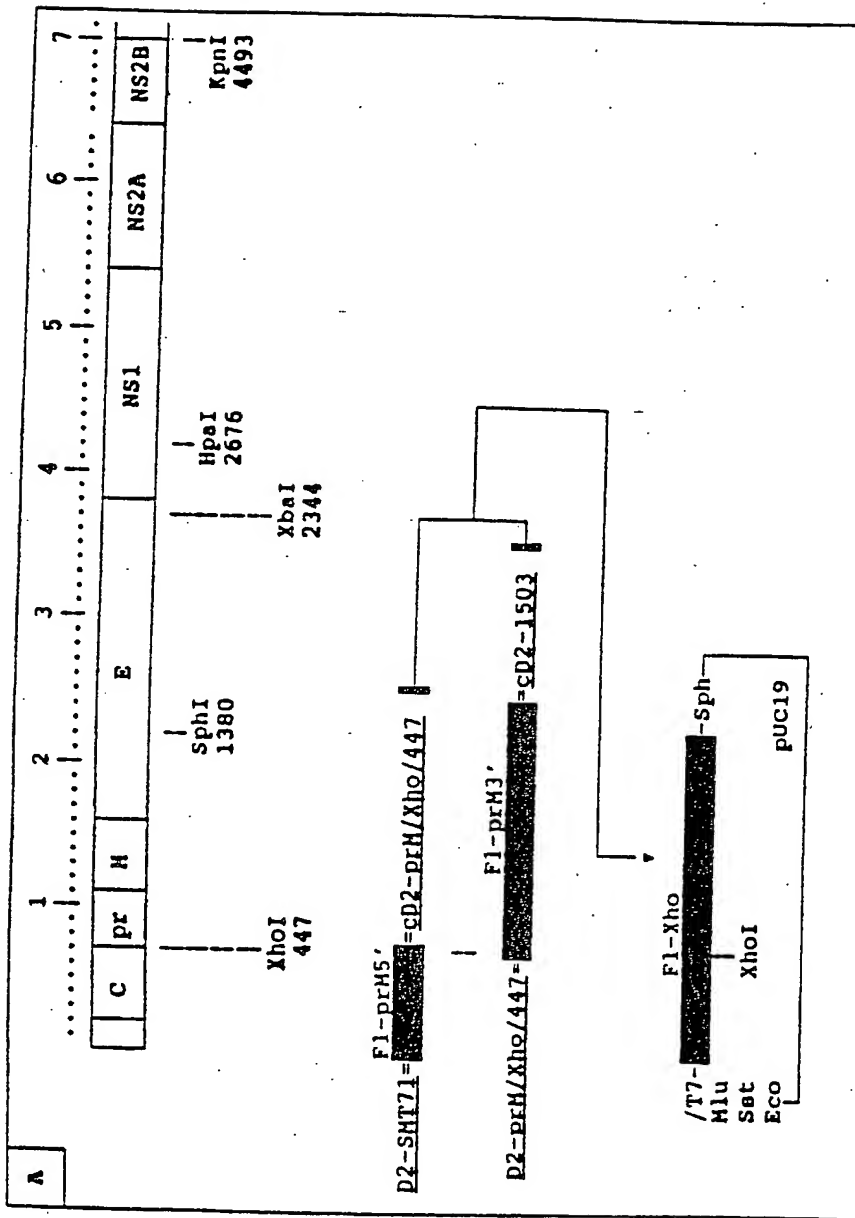


FIGURE 35A

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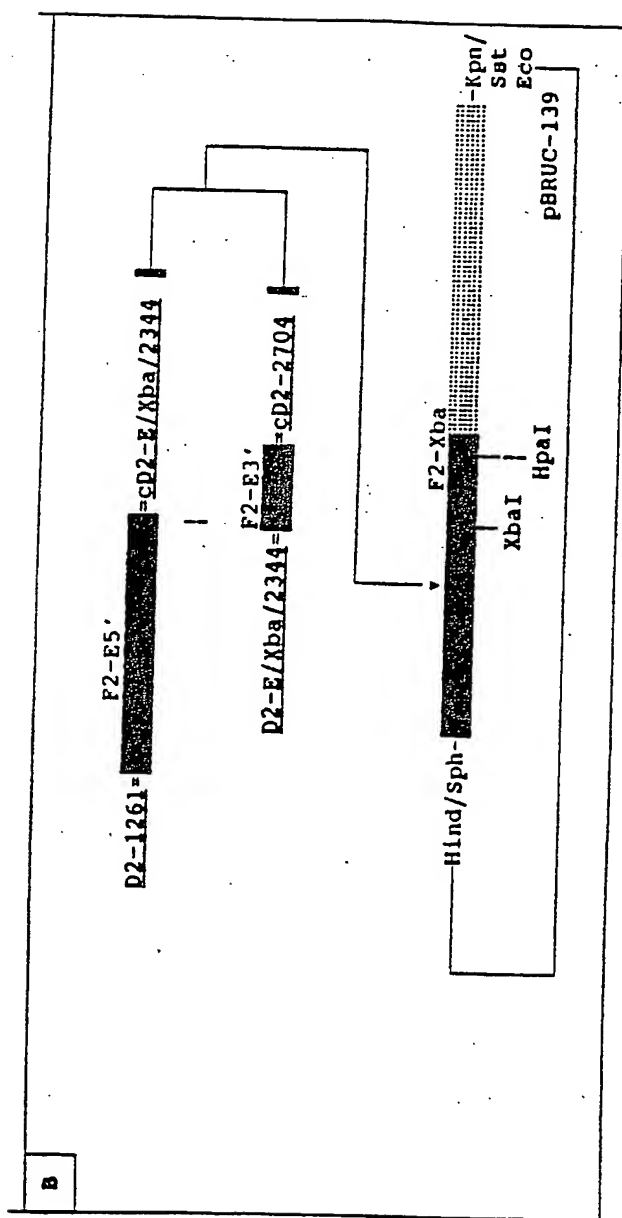
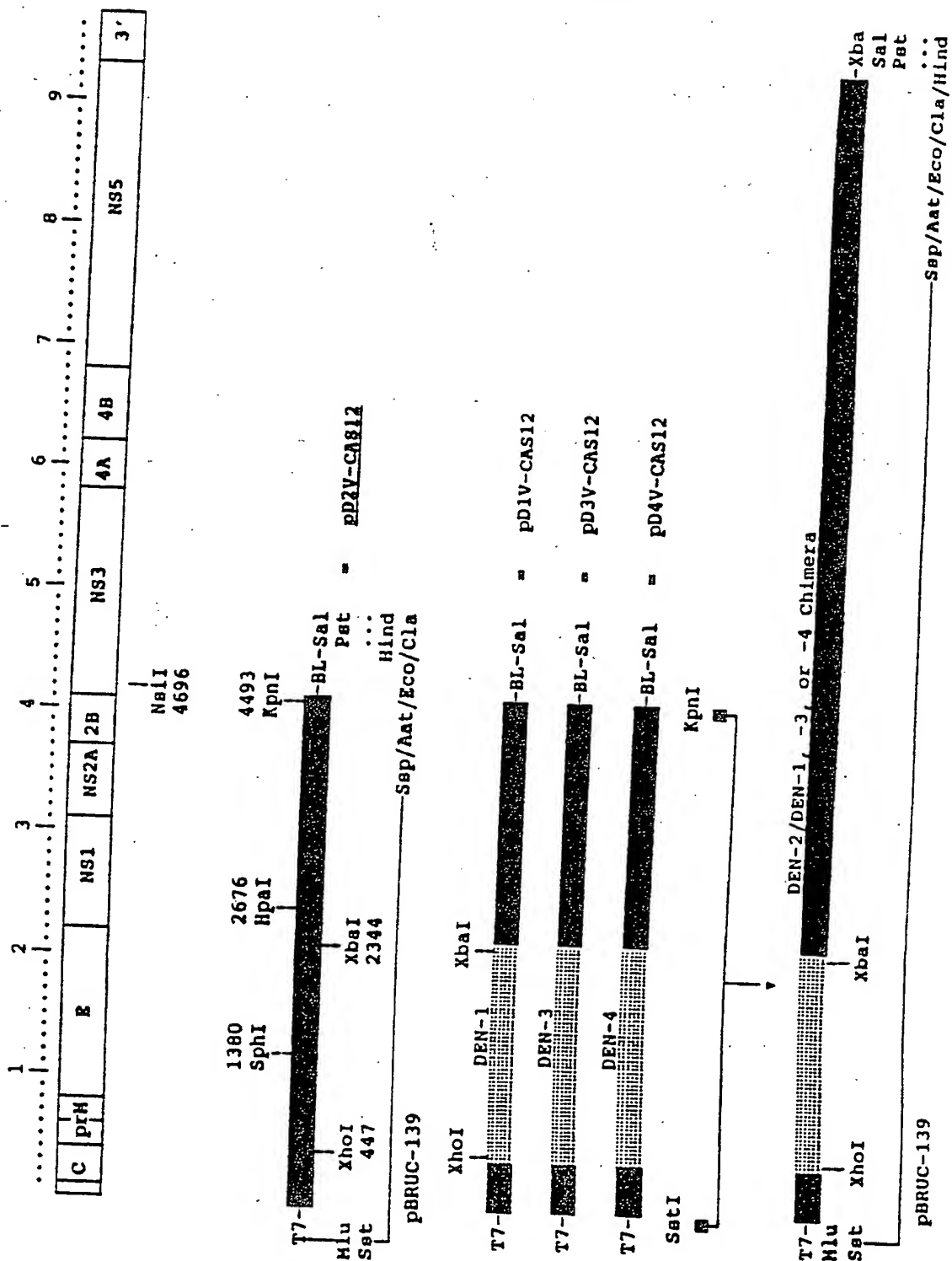


FIGURE 35B



INTERNATIONAL SEARCH REPORT

International Application No

PLI/US 96/09209

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/40 C12N15/86 C07K14/18 A61K39/12 C12N7/01
C12N7/00 C12N5/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	VACCINE, vol. 14, no. 4, March 1996, GUILDFORD GB, pages 329-336, XP000579824 VAUGHN, D.W. ET AL.: "Testing of a Dengue 2 live-attenuated vaccine (strain 16681 PDK 53) in ten american volunteers" see the whole document	1
X	VIROLOGY, vol. 187, no. 4, April 1992, ORLANDO US, pages 573-590, XP000601641 BLOK, J. ET AL.: "Comparaison of Dengue -2 virus and its candidate vaccine derivative: sequence relationships with the Flaviviruses and other viruses" see the whole document	7-12, 22-29,36
Y	---	1
	--- -/--	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

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Date of the actual completion of the international search

6 September 1996

Date of mailing of the international search report

23. 10. 96

Name and mailing address of the ISA

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Authorized officer

Chambonnet, F

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 96/09209

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO,A,93 06214 (US ARMY) -1 April 1993 see claims 40,63-68 ---	1
A	AMERICAN JOURNAL OF TROPICAL MEDICINE AND HYGIENE, vol. 47, no. 4 sup, 1992, pages 99-100; XP000600344 VAUGHN, D.W. ET AL.: "Phase I testing of a dengue-2 live-attenuated vaccine strain 16681 PDK 53 in american volunteers" see the whole document & 41st Annual Meeting of the American Society of Tropical Medicine and Hygiene Washington, USA November 15-19 1992 ---	1
A	WO,A,92 03161 (US GOVERNMENT) 5 March 1992 see the whole document ---	1
A	WO,A,93 22440 (UNIV SINGAPORE ;TAN YIN HWEE (SG); FU JIANLIN (SG); TAN BOON HUAN) 11 November 1993 see the whole document ---	1,2,5,6, 13
A	WO,A,92 03545 (VIROGENETICS CORP) 5 March 1992 see claims 1,9,10,16-23,26; example 13 ---	1
A	VIROLOGY, vol. 174, no. 2, February 1990, ORLANDO US, pages 479-493, XP002012813 RICO-HESSE, R.: "Molecular evolution and distribution of Dengue Viruses type 1 and 2 in nature" see the whole document ---	1
A	JOURNAL OF GENERAL VIROLOGY, vol. 69, no. 6, June 1988, pages 1391-1398, XP000600928 GRUENBERG, A. ET AL.: "Partial nucleotide sequence and deduced amino acid sequence of the structural proteins of Dengue virus type 2, New Guinea C and PU0-218 strains" see the whole document ---	1
	-/--	

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 96/09209

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>VIROLOGY, vol. 162, no. 1, January 1988, ORLANDO US, pages 167-180, XP000600931 HAHN, Y.S. ET AL.: "Nucleotide sequence of Dengue 2 RNA and comparison of the encoded proteins with those of other flaviviruses" see the whole document -----</p>	1

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 96/09209

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 6
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although this claim is directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 96/09209

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A-9306214	01-04-93	AU-B- 667836	18-04-96
		AU-B- 2691492	27-04-93
		CA-A- 2116980	01-04-93
		EP-A- 0604566	06-07-94
		JP-T- 6511150	15-12-94

WO-A-9203161	05-03-92	AU-B- 8762591	17-03-92
		US-A- 5494671	27-02-96

WO-A-9322440	11-11-93	AU-B- 4257593	29-11-93
		CA-A- 2134666	11-11-93
		EP-A- 0638122	15-02-95

WO-A-9203545	05-03-92	US-A- 5514375	07-05-96
		AU-B- 657711	23-03-95
		AU-B- 8728791	17-03-92
		GB-A,B 2269820	23-02-94
		JP-T- 6503227	14-04-94

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